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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 80.4786 Seconds

(without alignments) 3085.293 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571
Sequence: 1.gagctccgagatgaccagtc.....ggaccagctgagatcaaa 321

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p_model -DEV=xip
-O=/cgn2.1/USPTO_spool_p/US09403107/runat_29082005_120124_18882/bpp_query.fasta_1.1038
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HAPSPZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09403107@cgn_1_1_308@runat_29082005_120124_18882 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq_16dec04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003s:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	96.1	107	2	AAW80814 Amino aci
2	549	96.1	107	2	AAW80814 Amino aci
3	482	84.4	107	2	AAW80817 Amino aci
4	482	84.4	523	3	AAW44994 HD70scFv-
5	482	84.4	524	3	AAW44995 HD70scFv-
6	466	81.6	107	2	AAW54260 Anti-HIV
7	466	81.6	107	2	AAW01283 VL region
8	466	81.6	107	3	AAW98244 Anti-gp12
9	466	81.6	107	3	AAW95135 Anti-gp12
10	465	81.4	107	8	ADP22402 Human ant

11	465	81.4	108	8	ADP47294 Human rho
12	465	81.4	132	2	AAW22842 Human ant
13	464	81.3	107	4	AAW93644 Human ant
14	464	81.3	107	6	ABO27451 Anti-Rh (D
15	464	81.3	108	6	ABP96009 HSA anti-b
16	464	81.3	108	8	ADL92386 Anti-HSA
17	464	81.3	108	8	ADP47113 Human rho
18	464	81.3	108	8	ADQ14601 Single-de
19	464	81.3	108	8	ADQ77191 Dummy VK
20	464	81.3	108	8	ADQ77181 VK dummy
21	464	81.3	108	8	ADQ90912 VK/Ck pro
22	464	81.3	108	8	ADG78333 Vkapra du
23	464	81.3	108	8	ADG78331 Dpkappa9-
24	464	81.3	240	2	AAW02472 A single
25	464	81.3	240	4	AAW46007 Human MUC
26	464	81.3	240	4	AAW46038 Human TF
27	464	81.3	240	4	AAW46008 Human MUC
28	464	81.3	240	4	AAW46006 Human MUC
29	464	81.3	240	4	AAW46005 Human MUC
30	464	81.3	240	6	ABP95997 Human ber
31	464	81.3	240	6	ADL92369 Human pha
32	464	81.3	240	8	ADQ77165 HSA Heavy
33	463	81.1	108	8	ADP47299 Human rho
34	463	81.1	111	4	AAW63656 Amino aci
35	463	81.1	111	6	ABJ38615 Hepatic tis
36	463	81.1	214	8	ADR23360 Human CD7
37	463	81.1	214	8	ADR23358 Human CD7
38	463	81.1	214	8	ADR23366 Human CD7
39	463	81.1	214	8	ADR23364 Human CD7
40	463	81.1	240	6	ABJ38595 Hepatic tis
41	463	81.1	299	4	AAW63660 Amino aci
42	462	80.9	108	6	AAW16706 Human ant
43	462	80.9	240	4	AAW46010 Human MUC
44	462	80.9	245	8	ADR28069 NPb polyP
45	461	80.7	114	2	AAW13922 Light cha

ALIGNMENTS

RESULT 1	AAW80814 standard; protein; 107 AA.
AAW80814	
AC	AAW80814;
DT	16-FEB-1999 (first entry)
XX	
XX	
DE	Amino acid sequence of human Kappa 8 light chain variable region.
XX	
KW	Human; kappa 8 light chain variable region; receptor; antigen; tumour;
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;
KW	endocrine disease; degenerative disease.
XX	
OS	Homo sapiens.
XX	
PN	W09846645-A2.
XX	
PD	22-OCT-1998.
XX	
PF	14-APR-1998; 98WO-EP002180.
XX	
XX	14-APR-1997; 97EP-00106109.
PA	(KUFER/) KUFER P.
PA	(RAUM/) RAUM T.
XX	
PI	Kufer P, Raum T;
XX	
DR	WPI; 1998-594564/50.
DR	N-PSDB; AAW68536.
XX	
PT	Production of anti-human antigen receptors - by selecting a combination of functionally rearranged VH and VL immunoglobulin chains expressed from

PT a recombinant vector.
XX
XX Claim 9; Fig 6; 84pp; English.
PS
XX This is the protein sequence of the human kappa 8 light chain variable
CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 1.39e-50 Length: 107
Score: 549.00 Matches: 105
Percent Similarity: 98.13% Conservative: 0
Best Local Similarity: 98.13% Mismatches: 2
Query Match: 96.15% Indels: 0
DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x AAW80814 (1-107)
QY 1 GAGCTCCAGATGACCCGATCTCCATCTCTGTCGTCGAGACAGATGAC 60
DB 1 GluLeuGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 61 ATCACTTGTCGACCAAGTCAGACATTAGCAGCTATTAAATTGGTATCAGCAAAACA 120
DB 21 IleThrCysArgThrSerGlnSerIleSerSerTyrlleuAsnTrpTyrGlnGlnIysPro 40
QY 121 GACAGCCTCTTAAGCTGCTCATTTACTGCGATCTAACCCGGGAATCCGGGGTCCCTGAC 180
DB 41 GlyGlnProProIysLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 60
QY 181 CGATTGTCGACGCGGCTCTGCGACAGATTTCATCTTCACCTTCAGCATCTACAACT 240
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
DB 81 GluAspSerAlaThrTyrTyrCysGlnGlnSerTyrAspIleProTyrThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 101 GlyThrIysLeuGlnIleIys 107

RESULT 2
AAW17955
ID AAW17955 standard; protein; 107 AA.
XX
AC AAW17955;
XX
DT 04-AUG-1999 (first entry)
XX
DE Human kappa 8 light chain variable region.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KM autoimmune disease; scfv-antibody; single-chain Fv.
XX
OS Homo sapiens.
XX
PN WO925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.

XX
PI Kufer P, Raum T, Borschert K, Zetcl F, Lutterbuese R;
XX
XX WPI; 1999-338004/28.
DR N-PSDB; AAX77237.
XX
PT Phage display system for identification of binding site domains retaining
XX capacity to bind an epitope.
PS
XX Disclosure; Fig 3.2; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. Scfv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 1.39e-50 Length: 107
Score: 549.00 Matches: 105
Percent Similarity: 98.13% Conservative: 0
Best Local Similarity: 98.13% Mismatches: 2
Query Match: 96.15% Indels: 0
DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x AAW17955 (1-107)
QY 1 GAGCTCCAGATGACCCGATCTCCATCTCTGTCGTCGAGACAGATGAC 60
DB 1 GluLeuGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 61 ATCACTTGTCGACCAAGTCAGACATTAGCAGCTATTAAATTGGTATCAGCAAAACA 120
DB 21 IleThrCysArgThrSerGlnSerIleSerSerTyrlleuAsnTrpTyrGlnGlnIysPro 40
QY 121 GACAGCCTCTTAAGCTGCTCATTTACTGCGATCTAACCCGGGAATCCGGGGTCCCTGAC 180
DB 41 GlyGlnProProIysLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 60
QY 181 CGATTGTCGACGCGGCTCTGCGACAGATTTCATCTTCACCATCTACAACT 240
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
DB 81 GluAspSerAlaThrTyrTyrCysGlnGlnSerTyrAspIleProTyrThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 101 GlyThrIysLeuGlnIleIys 107

RESULT 3
AAW80817
ID AAW80817 standard; protein; 107 AA.
XX
AC AAW80817;
XX
DT 16-FEB-1999 (first entry)
XX

DE	Amino acid sequence of human kappa 5.1 light chain variable region.
KM	Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;
KM	endocrine disease; degenerative disease.
OS	Homo sapiens.
XX	
XX	MO9846645-A2.
PN	
PD	22-OCT-1998.
XX	
PF	14-APR-1998; 98WO-EP002180.
XX	
FR	14-APR-1997; 97EP-00106109.
XX	
PA	(KUFE/) KUFER P.
XX	(RAUM/) RAUM T.
PI	
XX	Kuifer P, Raum T;
DR	WPI, 1998-594564/50.
DR	N-PSDB; AAV68539.
PT	Production of anti-human antigen receptors - by selecting a combination
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from
XX	a recombinant vector.
PS	Claim 9; Fig 9; 84pp; English.
XX	
CC	This is the amino acid sequence of the human kappa light chain variable
CC	region, used in the method of the invention. for providing receptors that
CC	can be used for targeting antigens in humans without being immunogenic
CC	themselves. Such receptors can be used for treating diseases such as
CC	tumours or auto-immune diseases, graft rejection after transplantation,
CC	infectious diseases by targeting cellular receptors as well as allergic,
CC	inflammatory, endocrine and degenerative diseases by targeting key
XX	molecules involved in the pathological process
SQ	Sequence 107 AA;
Alignment Scores:	
Pred. No.:	2.47e-43 Length: 107
Score:	482.00 Matches: 92
Percent Similarity:	92.52% Conservative: 7
Best Local Similarity:	85.98% Mismatches: 8
Query Match:	84.41% Indels: 0
DB:	2 Gaps: 0
US-09-403-107-141 (1-321) x AAW80817 (1-107)	
OY	1 GAGCTCCAGATGACGCCAGTCTGCATTCCTCCTGTGTTCTGTGGGAGACAGAGTCACC 60
Ddb	1 GULBUGLMERHETHGLINSETPROBSERLEUSERALASERVALGYLSPARGVAITTHr 20
OY	61 ATCACTTGCGGACAAGTCAGACGATTACGAGCTAATAAATTGTATCAGAGAACA 120
Ddb	21 ILETHTCYBARGALASERGINSERILESSERTYLEUASNTIPRYGLNGNLNUPRO 40
OY	121 GGACGAGCTCTTAAGCTGCTCATTTACTG3CGCATTCACCCGGGAATCCGGGGTCCCTGAC 180
Ddb	41 GLYGINPROProLYSLEULEUILERYTRPALASERTHRARGLSUGERGIVALPPOSEP 60
OY	181 CGATTCAAGGGAGGGGGCTGTGGGAGAAATTCATCTCACATTCAGTCAGGCTCAACCT 240
Ddb	61 ARGPIESERGILSERGLUBERGILYNHAENTYRTHLNTHRLLESERLEUGLNPRO 80
OY	241 GAAGATTCTGCAACTTACTACTGTCTGACAGAGATTACGACATCCCGTACATTTGGCCAG 300
Ddb	81 GIUAEPHEIALATHRTYRHCYSGLINGINSERAPSERLEUPROLIETHRPHEGLYGLN 100
OY	301 GGGACCAAGCTGGAGATCAA 321

Db	101 GlythArgLeuAspIleGln 107
RESULT 4	
AAV44994	
ID	AAV44994 standard; protein; 523 AA.
XX	
AC	AAV44994;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	HD70scFv-CH1-GM-CSF chain.
XX	
KM	HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;
XX	
KM	epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
XX	
KM	granulocyte/macrophage colony stimulating factor; heterom antibody;
XX	
KM	CH1-domain; multifunctional compound; heavy chain constant domain;
XX	
KM	immunoglobulin; cytosolic; immunostimulatory; antileukemia; diagnosis;
XX	
KM	antiproliferative; prevention; treatment; malignant; haematopoietic cell;
XX	
KM	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX	
OS	Homo sapiens.
XX	
PN	WO200006605-A2.
XX	
PD	10-FEB-2000.
XX	
PF	28-JUL-1999; 99WO-EP005416.
XX	
PR	28-JUL-1998; 98EP-00114082.
XX	
PA	(MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX	
PI	Kuifer P, Dreier T, Baerle PA, Borschert K, Zettl F;
XX	
DR	WPI: 2000-195265/17.
XX	
DR	N-PSDB; AA250587.
XX	
PT	New multifunctional compounds useful for preventing and/or treating
XX	
PT	malignant cell growth and for detection and diagnosis.
XX	
BS	Example 10; Fig 55A; 166pp; English.
XX	
CC	The patent discloses heterom antibodies which are multifunctional compounds
XX	
CC	produced in a mammalian host cell as a secretable and fully functional
XX	
CC	heterodimer of two polypeptide chains, where one of the polypeptide
XX	
CC	chains comprises a CH1-domain (constant domain of an immunoglobulin
XX	
CC	heavy chain) and the other chain comprises CL-domain (constant domain of
XX	
CC	an immunoglobulin light chain). The polypeptide chains further comprise,
XX	
CC	fused to the constant domains at least two (poly)peptides having
XX	
CC	different receptor or ligand functions, where further at least two of the
XX	
CC	different (poly)peptides lack an intrinsic affinity for one another and
XX	
CC	are linked via the constant domains. The heterom antibodies have
XX	
CC	cytostatic, immunostimulatory, antileukemia and antiproliferative
XX	
CC	activities. These compounds can be used for diagnosing, preventing and
XX	
CC	treating malignant cell growth related to malignancies of haematopoietic
XX	
CC	cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
XX	
CC	melanomas and sarcomas. The present sequence is the left chain of a
XX	
CC	heterom antibody comprising HD70 single-chain Fv (scFv) fragment N-
XX	
CC	terminally linked to human CH1 domain which bears at its C-terminus the
XX	
CC	human inflammatory cytokine granulocyte/macrophage colony stimulating
XX	
CC	factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
XX	
CC	HD70 scFv specifically recognises the human epithelial cell adhesion
XX	
CC	molecule (EPCAM) also called 17-1A antigen
XX	
SO	Sequence 523 AA;
XX	
Alignment Scores:	
Pred. No.:	3,13e-43
Score:	482.00
Percent Similarity:	92.52%
Best Local Similarity:	85.98%
Query Match:	84.41%
DB:	3
	0
	Gaps:
	0

US-09-403-107-141 (1-321) x AAY44995 (1-523)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTCACC 60

DB 20 GltLeuGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 39

QY 61 ATCACTTGTCGACAGTGCAGCATTTAGAGCTAATTAATAATGGTATCAGCAAAACCA 120

DB 40 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnPro 59

QY 121 GGAAGCTCTCTAAGCTGCTCATTTACTGTGCGATCTAACCCGGGAATCCGGGCTCCCTGAC 180

DB 60 GlyGlnProProLysLeuLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 79

QY 181 CGATTACGTGGCAGCGGGTCTGGAGACAGATTTCACCTGCACATCAGCACTTCACACT 240

DB 80 ArgPheSerGlySerGlnSerGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnPro 99

QY 241 GAGATTCGTGCAACTTACTACTGTGTCAGAGAGTTAGACATCCCGTACCTTTTGGCCAG 300

DB 100 GlnAspPheAlaThrTyrPheCysGlnGlnSerAspSerLeuProIleThrPheGlyGln 119

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 120 GlyThrArgLeuAspIleGln 126

RESULT 5

AAY44995

ID AAY44995 standard; protein; 524 AA.

AC AAY44995;

XX

DT 23-MAY-2000 (first entry)

XX

DE HD70scFv-CK-interleukin 2.

XX

KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;

KM B2CMA; epithelial cell adhesion molecule; inflammation cytokine; IL-2;

KW interleukin-2; Ck-domain; kappa light chain constant domain;

KM heteromultibody; multifunctional compound; immunoglobulin; cytostatic;

KW immunostimulatory; antileukaemia; diagnosis; prevention;

KM antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;

KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

XX

OS Homo sapiens.

XX

PN WO200006605-A2.

XX

PD 10-FEB-2000.

XX

PF 28-JUL-1999; 99WO-EP005416.

XX

PR 28-JUL-1998; 98EP-00114082.

XX

PA (MICR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.

XX

PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;

XX

DR WPI; 2000-195265/17.

XX

DR N-PSDB; AAZ50588.

XX

PT New multifunctional compounds useful for preventing and/or treating

PT malignant cell growth and for detection and diagnosis.

XX

PS Example 10; Fig 55B; 166p; English.

XX

CC The patent discloses heteromultibodies which are multifunctional compounds

CC producible in a mammalian host cell as a secretable and fully functional

CC heterodimer of two polypeptide chains, where one of the polypeptide

CC chains comprises a CH1-domain (constant domain of an immunoglobulin

CC heavy chain) and the other chain comprises CH-domain (constant domain of

CC an immunoglobulin light chain). The polypeptide chains further comprise,

CC fused to the constant domains at least two (poly)peptides having

CC different receptor or ligand functions, where further at least two of the

CC different (poly)peptides lack an intrinsic affinity for one another and

CC are linked via the constant domains. The heteromultibodies have

CC cytostatic, immunostimulatory, antileukaemia and antiproliferative

CC activities. These compounds can be used for diagnosing, preventing and

CC treating malignant cell growth related to malignancies of haematopoietic

CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,

CC melanomas and sarcomas. The present sequence is the right chain of a

CC heteromultibody comprising HD70 single-chain Fv (scFv) fragment N-

CC terminally linked to human Ck domain (constant domain of immunoglobulin-

CC kappa light chain) which bears at its C-terminus the human inflammatory

CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the

CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX

SO Sequence 524 AA;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score:	3,13e-43	524	92
Percent Similarity:	482.00		92.52%
Best Local Similarity:	92.52%		8
Query Match:	85.98%		0
DB:	84.41%		0
	Gaps:		0

US-09-403-107-141 (1-321) x AAY44995 (1-524)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTCACC 60

DB 20 GltLeuGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 39

QY 61 ATCACTTGTCGACAGTGCAGCATTTAGAGCTAATTAATAATGGTATCAGCAAAACCA 120

DB 40 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnPro 59

QY 121 GGAAGCTCTCTAAGCTGCTCATTTACTGTGCGATCTAACCCGGGAATCCGGGCTCCCTGAC 180

DB 60 GlyGlnProProLysLeuLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 79

QY 181 CGATTACGTGGCAGCGGGTCTGGAGACAGATTTCACCTGCACATCAGCACTTCACACT 240

DB 80 ArgPheSerGlySerGlnSerGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnPro 99

QY 241 GAGATTCGTGCAACTTACTACTGTGTCAGAGAGTTAGACATCCCGTACCTTTTGGCCAG 300

DB 100 GlnAspPheAlaThrTyrPheCysGlnGlnSerAspSerLeuProIleThrPheGlyGln 119

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 120 GlyThrArgLeuAspIleGln 126

RESULT 6

AAR54260

ID AAR54260 standard; protein; 107 AA.

AC AAR54260;

XX

DT 25-MAR-2003 (revised)

XX

DT 10-NOV-1994 (first entry)

XX

DE Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain; variable region;

KW framework; complementarity determining region.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..21

FT Region /label= FRI

FT Region 22..33

FT Region /label= CDR1

Query Match: 81.61% Indels: 0
DB: 2 Gaps: 0
US-09-403-107-141 (1-321) x AAM01283 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTCTGTTGTGGAGACAGAGTCAACCATCACT 66
DB : : : : :
1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCTGACATTTAGAGCTATTAAATTGTTATCAGCGAACCAGACAG 126
DB : : : : :
21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLys 40

QY 127 CCTCTAGCTGCTCATTTCTGTCGATCTACCCGAGTCCGGGTCCTGACCGCATTC 186
DB 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGCGGCTGTGGACAGATTTCATCTCAACCATCAGAGTCTTACAACTGAAGAT 246
DB 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 80

QY 247 TCTGCACTTACTACTGTCTGACGACAGTTACGACATCCCGTACACTTTTGGCCAGGGGACC 306
DB 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
DB 101 LysLeuGlnIleLys 105

RESULT 8
ID AAY98244
XX AAY98244 standard; protein; 107 AA.
XX
AC AAY98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX
XX Homo sapiens.
XX
XX AUY948754-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-246867/22.
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence

CC (which does not comprise the sequence represented by AAY98206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
XX SQ Sequence 107 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1.33e-41 Length: 107
XX Score: 466.00 Matches: 90
XX Percent Similarity: 90.48% Conservative: 5
XX Best Local Similarity: 85.71% Mismatches: 10
XX Query Match: 81.61% Indels: 0
XX DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x AAY98244 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTCTGTTGTGGAGACAGAGTCAACCATCACT 66
DB : : : : :
1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCTGACATTTAGAGCTATTAAATTGTTATCAGCGAACCAGACAG 126
DB : : : : :
21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLys 40

QY 127 CCTCTAGCTGCTCATTTCTGTCGATCTACCCGAGTCCGGGTCCTGACCGCATTC 186
DB 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGCGGCTGTGGACAGATTTCATCTCAACCATCAGAGTCTTACAACTGAAGAT 246
DB 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 80

QY 247 TCTGCACTTACTACTGTCTGACGACAGTTACGACATCCCGTACACTTTTGGCCAGGGGACC 306
DB 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
DB 101 LysLeuGlnIleLys 105

RESULT 9
ID AAY95135
XX AAY95135 strand; protein; 107 AA.
XX
XX AAY95135;
XX
XX 30-JUN-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW

```
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX Homo sapiens.
OS
XX AU948756-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX (SCRI ) SCRIPPS RES INSTR.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-293393/26.
XX
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX
XX Example 9; Fig 11; 366pp; English.
XX
XX The present sequence represents a fragment of an anti-human
XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an
XX in vitro virus infectivity assay by 50%, at a concentration of less than
XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and
XX immunotherapy of HIV induced disease. They are useful as neutralising
XX field isolates and provide useful information regarding the
XX immunocompetence of an immune response in HIV infected patients. The
XX monoclonal antibodies are useful for producing anti-idiotypic antibodies
XX which can be used to screen human monoclonal antibodies to identify
XX whether the antibody has the same binding specificity as the antibodies
XX of the invention. The neutralising antibodies define new epitopes on the
XX HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
XX immunotherapeutic human monoclonal antibodies. A major advantages of the
XX monoclonal antibodies derives from the fact that they are encoded by a
XX human polynucleotide sequence. Thus in vivo use of the monoclonal
XX antibodies for diagnosis and immunotherapy of HIV induced disease greatly
XX reduces the problems of significant host immune response to the passively
XX administered antibodies which is a problem commonly encountered when
XX monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
XX An additional major advantage of the monoclonal antibodies described
XX derives from the fact that they immunoreact with a unique determinant
XX present on mature HIV glycoprotein gp120. This class of antibodies is
XX particularly effective at neutralising field isolates of HIV
XX
XX Sequence 107 AA;
SQ
Alignment Scores:
Pred. No.: 1,33e-41 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
DB: 3 Gaps: 0
US-09-403-107-141 (1-321) x AAY95135 (1-107)
QY 7 CAGATGACCCAGTCTCCATCTCTGCTGCTGTGGAGACAGATCCATCAT 66
DB 1 GluLeuThrGlnSerProSerSerLeuSerValGlyAAsPArgValThrIleThr 20
QY 67 TGTGGACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 126
DB 21 CysAlaGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGln 40
QY 127 CCTCTAGATGCTGCTATTACTGAGATCTACCCGGGAAATCCGGGGTCTGACCGATTC 186
DB 41 AlaProGlnSerLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
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```
QY 187 AGTGGACGGGGTCTGGGACAGATTTACTCTCATCCATCGAGTCTACCACTGAAGAT 246
DB 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyuAsp 80
QY 247 TCTGCACTTACTACTGCTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 306
DB 81 PheAlaThrTyrTyrGlnGlnSerTyrSerThrProTyrThrPheGlyGlnGlyThr 100
QY 307 AAGCTGAGATCAAA 321
DB 101 LysLeuGlnIleLeys 105
RESULT 10
ADP22402
ID ADP22402 standard; protein; 107 AA.
XX
XX ADP22402;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:308.
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
XX antibacterial; antiinflammatory; antiporiatic; antirheumatic;
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
XX prostrate cancer; immuno-mediated inflammatory disease;
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
XX reterosus; autoimmune disease; Crohn's disease; graft-host reaction;
XX septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX Homo sapiens.
XX
XX WO2004050683-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003MO-US038281.
XX
XX 02-DEC-2002; 2002US-0430729P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX Haak-Frendescho M, Rathnaswami P, Pigott C, Liang MW, Lee R;
XX Manchulenchko K, Fagiolini R, Senaldi G, Qiaojuan JS;
XX
XX WPI; 2004-480601/45.
XX
XX New recombinant human monoclonal antibody that specifically binds to
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX arthritis.
XX
XX Example 10; SEQ ID NO 308; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (1) that
XX specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFA in a patient sample, comprising contacting with
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX animal in need of treatment for the disease by administering the human
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[illegible]

QY	241	AAAGATTCTGCACCTTACTACGTGTAGACAGACTTCACATCCCGACCTTTTGSCCG	300
Db	103	GUAApheaIaThrTyrtYrtyeGIngeInserTyserThrProGInThrPheGlyGIn	122
QY	301	GGGACCAAGCTGGAGATCAAA	321
Db	123	GlyThrlYrYsValGluIleIys	129
RESULT 13			
ID	AAAG3644	standard; protein; 107 AA.	
AC	AAAG3644;		
XX	14-SEP-2001	(first entry)	
DE	Human anti-Rh(D) antibody clone SH13 protein sequence.		
XX	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;		
KW	red blood cell; Rh phenotype; diagnosis; therapeutic.		
XX	Homo sapiens.		
OS	US625455-B1.		
PN	03-JUL-2001.		
PD	29-JAN-1999;	99US-00240274.	
PF	11-OCT-1996;	96US-0028550P.	
PR	27-JUN-1997;	97US-00884045.	
PR	10-APR-1998;	98US-0081380P.	
XX	(UYBE-) UNIV PENNSYLVANIA.		
PA	Siegel DL;		
PI	WPI: 2001-388931/41.		
XX	N-PSDB; AAH68701.		
DR	New isolated protein, preferably a human anti-Rh(D) antibody for use in		
XX	diagnostics requiring a human instead of an animal antibody and in		
PT	therapeutic medicine.		
XX	Claim 1; Col 68; 162pp; English.		
PS	The present invention describes an isolated Rh(D) binding protein,		
XX	preferably a human antibody, (I) having an amino acid sequence comprising		
CC	one of the sequences (S) given in AA933558 to AA933669. (I) has		
CC	immunostimulant activity, and can be used as an immune system stimulant.		
CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies		
CC	are used in diagnostics that require human antibodies instead of animal		
CC	antibodies, such as determine the Rh phenotype of human red blood cells.		
CC	AAH68615 to AAH68726 represent the nucleotide sequence which encode		
CC	AA933558 to AA933669. AA933670 to AA933697 represent anti-Rh(D) heavy		
CC	chain CDR3 amino acid sequences which are given in the exemplification of		
CC	the present invention		
XX	Sequence 107 AA;		
Alignment Scores:			
	Pred. No.:	2.19e-41	Length: 107
	Score:	464.00	Matches: 90
	Percent Similarity:	89.52%	Conservative: 4
	Best Local Similarity:	85.71%	Mismatches: 11
	Query Match:	81.26%	Indels: 0
	DB:	4	Gaps: 0
US-09-403-107-141 (1-321) x AA933644 (1-107)			
QY	7	CAGATGACCCAGTCTGCATCTCCCTGTCGTCTGTGGAGACAGATCCATCACT	66
: : : : : :			

```

Db      2  GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 21
QY      67  TGTGGCAAGTCAAGACATTAGCAGCTATTAAATTGGATTCAGCAGAAACAGAGACAG 126
Db      22  CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlyLys 41
QY      127  CCTCCCTAAGCTGCTATTACTGTCGGCAGTCACCGGGAAATCCGGGGGCTCCGACCGATTG 186
Db      42  AlaProlyseuLeuLeuIleTyAlaAlaSerSerLeuArgSerGlyValProSerArgPhe 61
QY      187  AGTGGCAGCGGGTCTGGGACAGATTTCACCTCTCACCATCAGACGTCTACAACTGAAGAT 246
Db      62  SerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnProGluAsp 81
QY      247  TCTGCACACTTACTACTGTCTGACGAGAGTTACAGACATCCCGTACACTTTTGGCCAGGGACC 306
Db      82  PheAlaThrTyTrpCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 101
QY      307  AAGCTGGAGATCAAA 321
Db      102  LysLeuGlnIleLys 106

```

RESULT 14
ID ABO27451 standard; protein; 107 AA.

AC ABO27451;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH13.

KM Human; RH(D) binding protein; blood typing; blood product; antibody;
magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

XX N-PSDB; ACDA5365.

XX New human Rh(D)-binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 50; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX SQ Sequence 107 AA;

Alignment Scores:

Pred. No.: 2.19e-41 Length: 107
Score: 464.00 Matches: 90
Percent Similarity: 89.52% Conservative: 4
Best Local Similarity: 85.71% Mismatches: 11

Query Match: 81.26% Indels: 0
DB: 6 Gaps: 0

US-09-403-107-141 (1-321) x ABO27451 (1-107)

```

QY      7  CAGATGACCCAGTCTTCATCTCCCTGTCTGTCGTCTGTCGGAGACAGACTCACTACT 66
Db      2  GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 21
QY      67  TGTGGCAAGTCAAGACATTAGCAGCTATTAAATTGGATTCAGCAGAAACAGAGACAG 126
Db      22  CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlyLys 41
QY      127  CCTCCCTAAGCTGCTATTACTGTCGGCAGTCACCGGGAAATCCGGGGGCTCCGACCGATTG 186
Db      42  AlaProlyseuLeuLeuIleTyAlaAlaSerSerLeuArgSerGlyValProSerArgPhe 61
QY      187  AGTGGCAGCGGGTCTGGGACAGATTTCACCTCTCACCATCAGACGTCTACAACTGAAGAT 246
Db      62  SerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnProGluAsp 81
QY      247  TCTGCACACTTACTACTGTCTGACGAGAGTTACAGACATCCCGTACACTTTTGGCCAGGGACC 306
Db      82  PheAlaThrTyTrpCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 101
QY      307  AAGCTGGAGATCAAA 321
Db      102  LysLeuGlnIleLys 106

```

RESULT 15
ID ABP96009 standard; protein; 108 AA.

AC ABP96009;

DT 01-MAY-2003 (first entry)

DE HSA antibody related Vkappa chain Vkappa dummy.

KM Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;

KM antiinflammatory; antianemic; immunosuppressive; neuroprotective;

KM dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia;

KM inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease;

XX myasthenia gravis.

OS Homo sapiens.

PN Synthetic.

PN WO2003002609-A2.

XX 09-JAN-2003.

XX 28-JUN-2002; 2002WO-GB003014.

XX 28-JUN-2001; 2001GB-00015841.

XX (MEDT-) MEDICAL RES COUNCIL.

XX Winter G; Ignatovich O; Tomlinson I;

XX WPI; 2003-210246/20.

XX Dual-specific ligand having immunoglobulins with binding specificity to

PT different antigens or epitopes, useful for treating, preventing or

PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or

PT myasthenia gravis.

XX Example 1; Fig 3; 84pp; English.

The present invention describes a dual-specific ligand (I) comprising:

(a) a first single immunoglobulin variable domain with a binding

specificity to a first antigen or epitope; and (b) a second complementary

immunoglobulin single variable domain with a binding activity to a second

antigen or epitope. The binding domains are mutually complementary, and the first and second domains lack mutually complementary domains that share the same specificity. (1) has cytostatic, anti-HIV, antitumour, antiinflammatory, immunosuppressive and neuroprotective activities. The dual-specific ligand is useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia, inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's disease or myasthenia gravis). The dual-specific ligand may be used to recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is also useful for monitoring the efficacy of drugs, as well as for monitoring toxicity. The present sequence represents a human serum albumin (HSA) related antibody Vrapra sequence, which is used in an example from the present invention

SQ Sequence 108 AA;

Alignment Scores:	
Pred. No.:	2.19e-41
Score:	464.00
Percent Similarity:	89.72%
Best Local Similarity:	84.11%
Query Match:	81.26%
DB:	6
Length:	108
Matches:	90
Conservative:	6
Mismatches:	11
Indels:	0
Gaps:	0

US-09-403-107-141 (1-321) X ABP96009 (1-108)

QY	1	SAGGCTCAGATATACCCAGGCTCCATCTCCCTGTGGTCTCTGTGGAGACAGAGTACC	60
		
Db	1	AapIleGlnMetThrInserProSerSerLeuSerAlaSerValGlyAlaPheValThr	20
QY	61	ATCACTTGTTCGGACAAAGTCAGAGCACTTAGCAGCTATTAAATTTGGTATCGACGAAACCA	120
Db	21	IleThrCysArgAlaSerInserIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro	40
QY	121	GGACAGCCCTCTAGCTGCTCATTTACTGTGGCGCATCACCCGGAAATCCGGGGTCCCTGAC	180
		
Db	41	GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuInserGlyValProSer	60
QY	181	CGATTTCAGTGGCAGCGGGTCTGGGACAAAGATTTCACTCTCACCAATCAGCACTTACAACCT	240
Db	61	ArgPheSerGlySerIlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
QY	241	GAAGATTTCGCAACTTACTACTGTGACAGAGATTACGACATCCCGTACACTTTTGGCCAG	300
Db	81	GluAspPheAlaThrTyrTyrCysGlnGlnInserTyrSerThrProAsnThrPheGlyGln	100
QY	301	GGGACCAAGCTGAGATCAAA	321
		
Db	101	GlyThrLysValGlnIleLeuLys	107

Search completed: August 29, 2005, 11:37:15
Job time : 84.4786 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 17.1474 Seconds
(without alignments)
2794.861 Million cell updates/sec

Title: US-09-403-107-141
Perfect score: 571
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 1027090

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Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	81.6	107	1	US-08-276-852-104 Sequence 104, App
2	466	81.6	107	1	US-08-899-575-104 Sequence 104, App
3	466	81.6	107	1	US-08-899-575-104 Sequence 104, App
4	466	81.6	107	5	PCT-US95-08743-104 Sequence 104, App
5	464	81.3	107	3	US-09-240-274-156 Sequence 156, App
6	464	81.3	240	4	US-09-192-854-2 Sequence 2, Appli
7	463	81.1	109	3	US-09-157-370-3 Sequence 105, App
8	458	80.2	107	1	US-08-276-852-105 Sequence 105, App
9	458	80.2	107	1	US-08-899-575-105 Sequence 105, App
10	458	80.2	107	1	US-08-899-575-105 Sequence 105, App
11	458	80.2	107	5	PCT-US95-08743-105 Sequence 105, App
12	458	80.2	108	2	US-08-379-057-29 Sequence 29, Appl

13	457	80.0	107	3	US-09-240-274-175 Sequence 175, App
14	457	80.0	107	3	US-09-240-274-176 Sequence 176, App
15	455.5	79.8	108	3	US-09-240-274-32 Sequence 32, Appl
16	455.5	79.8	108	3	US-09-240-274-43 Sequence 43, Appl
17	455	79.7	107	3	US-09-240-274-37 Sequence 37, Appl
18	455	79.7	111	1	US-08-137-117D-67 Sequence 67, Appl
19	455	79.7	111	2	US-08-436-717-67 Sequence 67, Appl
20	455	79.7	126	1	US-08-137-117D-71 Sequence 71, Appl
21	455	79.7	126	2	US-08-436-717-71 Sequence 71, Appl
22	452.5	79.2	108	3	US-09-240-274-167 Sequence 167, App
23	452	79.2	127	3	US-08-836-561-71 Sequence 71, Appl
24	452	79.2	127	4	US-09-434-122-71 Sequence 71, Appl
25	452	79.2	134	3	US-08-718-323A-10 Sequence 10, Appl
26	452	79.2	134	4	US-09-587-526-10 Sequence 10, Appl
27	451	79.0	109	3	US-07-934-373C-3 Sequence 3, Appli
28	451	79.0	109	3	US-08-437-642B-3 Sequence 3, Appli
29	451	79.0	109	4	US-08-146-206C-3 Sequence 3, Appli
30	451	79.0	109	4	US-09-705-686-3 Sequence 3, Appli
31	451	79.0	109	4	US-09-705-392A-3 Sequence 3, Appli
32	451	79.0	109	4	US-09-705-398-3 Sequence 3, Appli
33	451	79.0	109	5	PCT-US93-07832-3 Sequence 3, Appli
34	451	79.0	127	3	US-08-284-516C-57 Sequence 57, Appl
35	451	79.0	127	4	US-09-537-911A-57 Sequence 57, Appl
36	451	79.0	214	2	US-07-934-373C-39 Sequence 39, Appl
37	451	79.0	214	3	US-08-437-642B-39 Sequence 39, Appl
38	451	79.0	214	5	PCT-US93-07832-39 Sequence 39, Appl
39	450	78.8	104	1	US-08-276-852-106 Sequence 106, App
40	450	78.8	104	1	US-08-899-575-106 Sequence 106, App
41	450	78.8	104	1	US-08-899-575-106 Sequence 106, App
42	450	78.8	104	5	PCT-US95-08743-106 Sequence 106, App
43	450	78.8	107	2	US-08-652-558-36 Sequence 36, Appl
44	450	78.8	107	2	US-08-378-939-14 Sequence 14, Appl
45	449	78.6	107	3	US-09-240-274-179 Sequence 179, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

Alignment Scores:
Pred. No.: 6.3e-49 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-276-852-104 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAGACGATTAGACGCTATTAAATTGGTATGACGAAACAGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInysProGlyLys 40

QY 127 CTTCCCTAAGCTGCTCACTTCTGCGCATCCCGGAAATCCGGGGTCCCTGACCGATTG 186
Db 41 AlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGACAGCGGCTCTGGAGACAGATTTCACCTCAGCATCAGACGATCAACCTGAAGAT 246
Db 61 SerGlySerIleSerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80

QY 247 TCTGCAACTTACTGTCAGACAGATTAGACATCCCGTACCTTTGGCCAGGGACC 306
Db 81 PheAlaThrTyTyCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 2
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbos, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Alignment Scores:
Pred. No.: 6.3e-49 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-104 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGAGTCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAGACGATTAGACGCTATTAAATTGGTATGACGAAACAGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInysProGlyLys 40

QY 127 CTTCCCTAAGCTGCTCACTTCTGCGCATCCCGGAAATCCGGGGTCCCTGACCGATTG 186
Db 41 AlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGACAGCGGCTCTGGAGACAGATTTCACCTCAGCATCAGACGATCAACCTGAAGAT 246
Db 61 SerGlySerIleSerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80

QY 247 TCTGCAACTTACTGTCAGACAGATTAGACATCCCGTACCTTTGGCCAGGGACC 306
Db 81 PheAlaThrTyTyCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 3
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbos, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 NO. 58044th Torrey Pines Road, Suite 220,
; STREET: Mail Drop 1PC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Alignment Scores:
Pred. No.: 6.3e-49 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-104 (1-107)
QY 7 CAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGATCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20
QY 67 TGTGGCAAGTGCAGACGATTAGCAGATTAATAATTGATATCGACAGAAACGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlnLys 40
QY 127 CCTCTAAGCTGCTCATTACTGTGGCATTAACCCGGGAATCCGGGGTCCCTGACCGATT 186
Db 41 AlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
QY 187 AGTGGACGGGGTCTGGAGACGATTTCATCTGACCATCAGCATGCTTCAACCTGAAGAT 246
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnLys 80
QY 247 TCTGCACTTACTACTGTCAGACAGATTAAGCATCCGTCACATTTTGGCAGGGAGCC 306
Db 81 PheAlaThrTyTyTyCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 100
QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

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RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Alignment Scores:
Pred. No.: 6.3e-49 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x PCT-US95-08743-104 (1-107)
QY 7 CAGATGACCCAGTCTCCATCTCTGCTGCTTGTGGAGACAGATCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20
QY 67 TGTGGCAAGTGCAGACGATTAGCAGATTAATAATTGATATCGACAGAAACGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlnLys 40
QY 127 CCTCTAAGCTGCTCATTACTGTGGCATTAACCCGGGAATCCGGGGTCCCTGACCGATT 186
Db 41 AlaProLysLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
QY 187 AGTGGACGGGGTCTGGAGACGATTTCATCTGACCATCAGCATGCTTCAACCTGAAGAT 246
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnLys 80
QY 247 TCTGCACTTACTACTGTCAGACAGATTAAGCATCCGTCACATTTTGGCAGGGAGCC 306
Db 81 PheAlaThrTyTyTyCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 100
QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 5
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29

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QY 121 GGACAGCTCTAGAGCTGCTATTACTGTCGAGATCCCGGAGATCCCGGCTCCCTGAC 180
 DB 41 GYLYSALALPRLYSLEULEULERYRPAALASERALEUGLISERGLYVALPROSER 60
 QY 181 CGATTTCAGTGGAGCGGCTGTGGAGACAGATTTCAGCTTCAGCATGAGCATGACACT 240
 DB 61 AGPHEISERGLYSERGLYSERGLYHRAPHEITHRILESERISERLEUGLIPRO 80
 QY 241 GAGAGTTCTGCACTTACTACTGTGACAGAGTTACGACATCCCGTACCTTTGGCCAG 300
 DB 81 GUAAEPHEALATHRYTCYSGINGINTYRYSERLEUPROTYRHPHEGLYGLN 100
 QY 301 GGGACAGCTGAGATCAAA 321
 DB 101 GYINRLYSVALGLNILEYS 107
 RESULT 8
 US-08-276-852-105
 ; Sequence 105, Application US/08276852
 ; Patent No. 5652138
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbos, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/276,852
 ; FILING DATE: 18-JUL-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCR1452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 105:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-276-852-105
 Alignment Scores:
 Pred. No.: 6 098-48 Length: 107
 Score: 458.00 Matches: 89
 Percent Similarity: 89.52% Conservative: 5
 Best Local Similarity: 84.76% Mismatches: 11
 Query Match: 80.21% Indels: 0
 DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-276-852-105 (1-107)
 QY 7 CAGATGACCCAGTCTCCATCCCTGCTGCTTCTGTGGAGACAGATGACATCACT 66
 DB 1 GLEUTHRGINSERPROSERSERLEUSERLASERVALGLYAPARGVALTHRILETHR 20
 QY 67 TGTGGACAGTCTGAGCATTTAGCACTTTAAATTGTATTCAGCAGAAACCGAGACG 126
 DB 21 CYSALGALASERGINSERLILESERISERLYRLEUSANTPYRGLINGLNLVSPROGLYLS 40
 QY 127 COTCTAAGCTGCTCATTTACTTACGAGATCCCGGAGATCCCGGCTCCCTGACCGATTTC 186
 DB 41 ALAPROYSLEULEULERYRALALASERISERLEUGLISERGLYVALPROSERARGPHE 60
 QY 187 AGTGCAGCGGCTGTGGAGACAGATTTCAGTTCAGCATGAGCATGACACTGAGAT 246
 DB 61 SERGLYSERGLYSERGLYTHRASPHEITHRILESERISERLEUGLIPROGLUNSP 80
 QY 247 TCTGCACTTACTACTGTGACAGAGTTACGACATCCCGTACCTTTGGCCAGGAGCC 306
 DB 81 PHEALATHRYTCYSGINGINSEXTYRISERTHRPROGINTHRPHGLYGLNGLYTHR 100
 QY 307 AAGCTGAGATCAAA 321
 DB 101 LYSLEUGLILEYS 105
 RESULT 9
 US-08-899-575-105
 ; Sequence 105, Application US/08899575
 ; Patent No. 5770440
 ; GENERAL INFORMATION:
 ; APPLICANT: Burton, Dennis R
 ; APPLICANT: Barbos, Carlos F
 ; APPLICANT: Lerner, Richard A
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 ; STREET: Mail Drop TPC8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,575
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; APPLICATION NUMBER: US 08/178,302
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/954,148
 ; FILING DATE: 30-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCR1452P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 105:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Alignment Scores:
Pred. No.: 6,096-48 Length: 107
Score: 458.00 Matches: 89
Percent Similarity: 89.52% Conservative: 5
Best Local Similarity: 84.76% Mismatches: 11
Query Match: 80.21% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-105 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGTGGAGACAGAGTCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAGACGATTAGCAGCTATTAATGTGATCAGCGAAGAACGAGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerIleuAsnTrpGlyGlnIlyProGlyLys 40

QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATCTACCCGGGATCCGGGGTCCCTGACCGATTG 186
Db 41 AlaProIySLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGGGGTCTGGGACAGATTTCAGTCTCAACATCAGAGTCTTACAACTGAAGAT 246
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyAsp 80

QY 247 TCTGGCAACTTACTCTGTCAGAGATTAGACATCCCGTACACTTTGGCCAGGGGACC 306
Db 81 PheAlaThrTyrTrpCysGlnGlnSerIleSerThrProGlnThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 10
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbias, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Alignment Scores:
Pred. No.: 6,096-48 Length: 107
Score: 458.00 Matches: 89
Percent Similarity: 89.52% Conservative: 5
Best Local Similarity: 84.76% Mismatches: 11
Query Match: 80.21% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-105 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGTGGAGACAGAGTCACCATCACT 66
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAGACGATTAGCAGCTATTAATGTGATCAGCGAAGAACGAGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerIleuAsnTrpGlyGlnIlyProGlyLys 40

QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATCTACCCGGGATCCGGGGTCCCTGACCGATTG 186
Db 41 AlaProIySLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGGGGTCTGGGACAGATTTCAGTCTCAACATCAGAGTCTTACAACTGAAGAT 246
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyAsp 80

QY 247 TCTGGCAACTTACTCTGTCAGAGATTAGACATCCCGTACACTTTGGCCAGGGGACC 306
Db 81 PheAlaThrTyrTrpCysGlnGlnSerIleSerThrProGlnThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 11
PCT-US95-08743-105
Sequence 105, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-105

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Alignment scores:	
Pred. No.:	6.09e-48
Score:	458.00
Percent Similarity:	89.52%
Best local Similarity:	84.76%
Query Match:	80.21%
DB:	5
Length:	107
Matches:	89
Conservative:	85
Mismatches:	11
Indels:	0
Gaps:	0

US-09-403-107-141 (1-321) X PCT-US95-08743-105 (1-107)

Qy	7	CAAGTATGCCAGTCTCATCTCCCTGCTGTGGTTCGTGGAGACAGAGTACCATCACT	66
		
Db	1	GlutethrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr	20
Qy	67	TGTTCGACAGTATGAGGACATTAGACGCTATTAAATTGGTATCAGCAGAAACCGAGCAG	126
Db	21	CyargValaSerGlnSerIleSerSerTyrlleuAsnTrpYrGlnGlnLysProGlyLys	40
Qy	127	CCCTCAAGCTGCTCATTTACTGCGCANTTACCCGGGATCCGGGGTCCCTGACCGGATT	186
Db	41	AlaProLysLeuLeuIleTyrlalAlaSerSerLeuGlnSerGlyValProSerArgPhe	60
Qy	187	AGTGGCAGCGGGGTCTGGGACAGATTTCATCTTCACCATCAGACAGTCTTCAACCTGAAGAT	246
Db	61	SerGlySerSerIleSerIlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnAsp	80
Qy	247	TCTGCACTACTACTACTGTCAGCAGAGTTACGACATCCCGTACCATTTTGGCCAGGGAGCC	306
Db	81	PheAlaThrTyrlTyrcyGlnGlnIleSerTyrlSerThrProGlnThrPheGlyGlnGlyThr	100
Qy	307	AAAGTCGAGATCAAA	321
Db	101	LysLeuGlnIleLys	105

RESULT 12
 US-08-379-057-29
 Sequence 29, Application US/08379057
 Patent No. 5876950
 GENERAL INFORMATION:
 APPLICANT: Siadak, Anthony W.
 APPLICANT: Hollenbaugh, Diane L.
 APPLICANT: Gilliland, Lisa K.
 APPLICANT: Gordon, Marcia L.
 APPLICANT: Bajorath, Jurgen
 APPLICANT: Aruffo, Alejandro A.
 TITLE OF INVENTION: Monoclonal Antibodies Specific For
 TITLE OF INVENTION: Differential Epitopes of Human gp39 and Methods For Their Use
 TITLE OF INVENTION: In Diagnosis and Therapy
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bristol-Myers Squibb Company
 STREET: 3005 First Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/379,057
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Poor Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3670
TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-29

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Alignment Scores:	
Pred. No.:	6,11e-48
Score:	458.00
Percent Similarity:	88.79%
Best local Similarity:	83.18%
Query Match:	80.21%
DB:	2
Length:	108
Matches:	89
Conservative:	6
Mismatches:	12
Indels:	0
Gaps:	0

US-09-403-107-141 (1-321) X US-08-379-057-29 (1-108)

Oy	1	GAGGTCCAGATGAGCCAGTCTTCATCTCCCTGATCGTCTTGCTGGAGAGACAGAGTACC	60
		::: ::::	
Db	1	AspIleGlnMetCtnrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20
Oy	61	ATCATCTTGTCGGACAACTCAGAGCATTTGACAGCTATTAAATTTGGTATCAGCAAAACCA	120
Db	21	IleThrCysAspGlnAspGlnSerIleSerSerTyrLeuAlanTrypticGlnIleHisPro	40
Oy	121	GGACAGCCTCTTAAGTCTCATTTACTGCGGATATCACCGGAAATCCGGGGTCCCTGAC	180
		::: ::::	
Db	41	GlyIysAlaProIysLeuIleuIleTyrAlaIaSerSerLeuGlnSerGlyAlaProSer	60
Oy	181	CGATTCACTGCGACGGGGCTTGGGACAGATTTCACTCTCACCATTACAGAGTTTACAACCT	240
Db	61	ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
Oy	241	GAAGATTCGCAACTTACTACTGTGCAGAGAGTTCAGCATTCCTGATCACTTTTGGCCAG	300
Db	81	GlnAspPheAlaThrTyrTyrCysGlnIleSerTyrSerThrProLeuThrPheGlyGly	100
Oy	301	GGAGCAAGCTGGAGATCAAA	321
Db	101	GlyThrIysValGlnIleIys	107

```

RESULT 13
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
; US-09-240-274-175

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Alignment Scores:

Pred. No.: 8.09e-48 Length: 107
Score: 457.00 Matches: 87
Percent Similarity: 90.48% Conservative: 8
Best Local Similarity: 82.86% Mismatches: 10
Query Match: 80.04% Indels: 0
DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x US-09-240-274-175 (1-107)

QY 7 CAGATGACCGAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66
Db 2 GtLeuThrGlnSerProSerSerLeuSerLeuValGlyAspArgValThrValThr 21
QY 67 TGTGGCAAGTCAGACGATTAGACGCTTAAATTGGTATCAGCAAGAACAGAGACG 126
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySerProGlyLys 41
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCAGCAAGAT 246
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81
QY 247 TGTGCAACTTACTGTCAGACGAGATTACGACATCCCGTACCTTTGGCCAGGGACC 306
Db 82 PheAlaThrTyTrpCysGlnGlnSerTySerThrProTrpPheGlyGlnGlyThr 101
QY 307 AAGCTGAGATCAAA 321
Db 102 LysValGluIleLys 106

RESULT 14

US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Alignment Scores:

Pred. No.: 8.09e-48 Length: 107
Score: 457.00 Matches: 87
Percent Similarity: 90.48% Conservative: 8
Best Local Similarity: 82.86% Mismatches: 10
Query Match: 80.04% Indels: 0
DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x US-09-240-274-176 (1-107)

QY 7 CAGATGACCGAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66
Db 2 GtLeuThrGlnSerProSerSerLeuSerLeuValGlyAspArgValThrValThr 21

QY 67 TGTGGCAAGTCAGACGATTAGACGCTTAAATTGGTATCAGCAAGAACAGAGACG 126
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySerProGlyLys 41
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCAGCAAGAT 246
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81
QY 247 TGTGCAACTTACTGTCAGACGAGATTACGACATCCCGTACCTTTGGCCAGGGACC 306
Db 82 PheAlaThrTyTrpCysGlnGlnSerTySerThrProTrpPheGlyGlnGlyThr 101
QY 307 AAGCTGAGATCAAA 321
Db 102 LysValGluIleLys 106

RESULT 15

US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32

Alignment Scores:

Pred. No.: 1.24e-47 Length: 108
Score: 455.50 Matches: 90
Percent Similarity: 89.62% Conservative: 5
Best Local Similarity: 84.91% Mismatches: 10
Query Match: 79.77% Indels: 1
DB: 3 Gaps: 1

US-09-403-107-141 (1-321) x US-09-240-274-32 (1-108)

QY 7 CAGATGACCGAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66
Db 2 GtLeuThrGlnSerProSerSerLeuSerLeuValGlyAspArgValThrValThr 21
QY 67 TGTGGCAAGTCAGACGATTAGACGCTTAAATTGGTATCAGCAAGAACAGAGACG 126
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySerProGlyLys 41
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCAGCAAGAT 246
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81
QY 247 TGTGCAACTTACTGTCAGACGAGATTACGACATC--CCGTACCTTTGGCCAGGGG 303

Db	82	PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProProTyrThrPheGlyGlnGly	101
Qy	304	ACCAAGCTGGAGATCAAA	321
Db	102	ThrTyrLeuGlnIleLeu	107

Search completed: August 29, 2005, 11:08:05
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 300.423 Seconds

(Without alignments)
839.678 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
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Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 3534298

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-MAXLEN=200000000 -USER=US09403107@cgn_1.260.@rnat_29082005.120126.18939
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Database : Published Applications AA.*

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22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	549	96.1	214	18	US-10-778-915-2
4	482	84.4	107	14	US-10-325-694-148
5	482	84.4	107	14	US-10-325-694-152
6	468	82.0	107	10	US-09-791-153A-67
7	466	81.6	107	14	US-10-016-986-104
8	465	81.4	107	17	US-10-727-155-308
9	465	81.4	108	17	US-10-726-332-209
10	464	81.3	107	10	US-09-848-798-156
11	464	81.3	108	16	US-10-409-814A-4
12	464	81.3	108	17	US-10-726-332-28
13	464	81.3	240	9	US-09-192-854-2
14	464	81.3	240	9	US-09-968-561A-2
15	464	81.3	240	10	US-09-968-744A-2
16	464	81.3	240	11	US-09-968-561A-2
17	464	81.3	240	16	US-10-744-774-1
18	463	81.1	108	17	US-10-726-332-214
19	463	81.1	108	17	US-10-805-177-64
20	463	81.1	111	14	US-10-203-754A-57
21	461	80.7	111	18	US-10-916-840-100
22	460	80.6	107	15	US-10-309-762-88
23	460	80.6	107	17	US-10-338-353-103
24	459	80.4	116	17	US-10-783-311-198
25	458	80.2	107	14	US-10-016-986-105
26	458	80.2	108	17	US-10-726-332-18
27	458	80.2	111	14	US-10-203-754A-56
28	457	80.0	107	10	US-09-848-798-175
29	457	80.0	107	10	US-09-848-798-176
30	457	80.0	107	15	US-10-309-762-68
31	457	80.0	107	15	US-10-309-762-68
32	457	80.0	108	16	US-10-744-774-13
33	455.5	79.8	108	10	US-09-848-798-32
34	455.5	79.8	108	10	US-09-848-798-43
35	455	79.7	107	10	US-09-848-798-37
36	455	79.7	108	16	US-10-798-380-20
37	455	79.7	108	17	US-10-726-332-26
38	455	79.7	108	17	US-10-477-830-90
39	455	79.7	126	18	US-10-837-904-64
40	455	79.7	126	18	US-10-837-904-68
41	454	79.5	108	17	US-10-726-332-22
42	454	79.5	108	17	US-10-805-177-20
43	453	79.3	106	15	US-10-377-121-5
44	453	79.3	109	16	US-10-745-775-2
45	453	79.3	109	16	US-10-783-730-2

ALIGNMENTS

RESULT 1
US-10-325-694-142
; Sequence 142, Application US/10325694
; Publication No. US200301463A1
; GENERAL INFORMATION:
; APPLICANT: KUPFER, PETER
; APPLICANT: RAMM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; PRIOR APPLICATION NUMBER: 2002-12-19
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN


```

Db      101 GlyThrLeuGlnIleLeys 107
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RESULT 4
US-10-325-694-148
; Sequence 148, Application US/10325694
; Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUPER, PETER
APPLICANT: RAUM, TOBIAS
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 148
LENGTH: 107
TYPE: PRT
ORGANISM: HUMAN
US-10-325-694-148

Alignment Scores:
Pred. No.: 6,7e-42 Length: 107
Score: 482.00 Matches: 92
Percent Similarity: 92.52% Conservative: 7
Best Local Similarity: 85.98% Mismatches: 8
Query Match: 84.41% Indels: 0
DB: 14 Gaps: 0

US-09-403-107-141 (1-321) x US-10-325-694-148 (1-107)
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DB      1 GtLeuGlnMeThrGlnSerProSerSerLeuSerAlaSerValGlySpaGValThr 20
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QY      61 ATCACTTGTGCGACAAGATGAGAGCATTTACAGCATTAATAAATGGTATGACGAAACCA 120
      |||||||
DB      21 IetHrCyArGAlaSerGlnSerIleSerSerTyrLeuSerValTyrGlnGlnSpPro 40
      |||
QY      121 GGACAGCCTCTTAAGCTGTCATTATTCGTGGCAGATCAACCCGGGAATCCGGGTCCTGAC 180
      |||||||
DB      41 GlyGlnProProIySerLeuLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 60
      |||
QY      181 CGATTTCAGTGGCAGCGGGTCTGTGGAGACGATTTACTCTCACCATTCAGCACTTACAACCT 240
      |||||||
DB      61 ArgPheSerGlySerGlnSerGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnPro 80
      |||
QY      241 GAAGATTTCGAACCTACTACTGTGTGACAGAGTTACGACATCCCGTCACTTTGGCCAG 300
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DB      81 GluAspPheAlaThrTyrPheCysGlnGlnSerAspSerLeuProIleThrPheGlyGln 100
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DB      101 GlyThrArgLeuAspIleGln 107
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RESULT 5
US-10-325-694-152
; Sequence 152, Application US/10325694
; Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUPER, PETER
APPLICANT: RAUM, TOBIAS
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14

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NUMBER OF SEQ ID NOS: 152		/		SOFTWARE: PatentIn Ver. 2.1		/		SEQ ID NO 152		/		LENGTH: 107		/		TYPE: PRT		/		ORGANISM: HUMAN		/		US-10-325-694-152	
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Pred. No.:		6,7e-42																							
Score:		482.00																							
Percent Similarity:		92.52%																							
Best Local Similarity:		85.98%																							
Query Match:		84.41%																							
DB:		14																							
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QY	1	GAGGTCCAGATGACCCAGTCCATCTCCCTGTCGCTCTGNGGGAGACAGATCACC	60																						
DB	1	GIUeuglInnetcInrgInserProserSerIuserIaservalGIyaspavqValthr	20																						
QY	61	ATCACTTGTCGCGACAGTCAGAGCATTCAGACGCTATTAAATTGGTACACAGAAACA	120																						
DB	21	IllethrCysarqalaserqInserIlleSerSerTyreIuasnTrpTyrgInqInlyPro	40																						
QY	121	GGACAGCCTCCTTAAGCTGCTCATTTACTGGCGATCTACCCGGAAATCCGGGGTCCCTGCAC	180																						
DB	41	GIyInPrpProIyIsleuIeulIeTyTrpIalaserThrIrgIuserGIyValProasp	60																						
QY	181	CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTCACCTCCACCATCAGACAGCTACACT	240																						
DB	61	ArgheSerqIyserqIuserGIyThraSnTyThrIeuThrIlleSerSerIeuqInPro	80																						
QY	241	GAGATTTCGCAACTTACTACTGTACAGAGATTTCAGACATCCCGTACACTTTGGCCAG	300																						
DB	81	GIuasphealatrThrTyPheCyqGIInqInseraspserIeuProIleThrPheGIyIn	100																						
QY	301	GGGACCAAGCTGGAGATCAAA	321																						
DB	101	GIyThrIrgIeuaspIleqIn	107																						
RESULT 6		US-09-791-153A-67																							
/ Sequence 67, Application US/09791153A																									
/ Publication No. US20030103978A1																									
/ GENERAL INFORMATION:																									
/ APPLICANT: Deshpande, Rajendra																									
/ APPLICANT: Hitez, Anna																									
/ APPLICANT: Boyle, William																									
/ APPLICANT: Sullivan, John																									
/ TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN																									
/ FILE REFERENCE: A-633A																									
/ CURRENT APPLICATION NUMBER: US/09/791,153A																									
/ CURRENT FILING DATE: 2001-07-17																									
/ PRIOR APPLICATION NUMBER: 09/511,139																									

US-09-403-107-141 (1-321) x US-09-791-153A-67 (1-107)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTCTGTGGAGACAGAGTCACC 60
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
QY 61 ATCACTTGTGGCAAGTTCAGACATTAGCAGCTAATTAATGATATCAGCAGAAACA 120
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnPro 40
QY 121 GAGACGCTCTTAACTGCTCATTTACTGTGGCATTAACCGGAATCCGGGTCCTGAC 180
Db 41 GlyLeuAlaProLysLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY 181 CGATTGAGTGGCAGCGGCTGTGGAGAGATTTCATCTCCATCCAGATCTACAACT 240
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCACTTACTACTGTGACAGAGATTACACATCCCGTACACTTTGGCCAG 300
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGln 100
QY 301 GGAACCAAGCTGGAGATCAA 321
Db 101 GlyThrIysValGluIleLys 107

RESULT 7

US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Alignment Scores:
Pred. No.: 3,22e-40 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x US-10-016-986-104 (1-107)

QY 7 CAGATGACCAAGTCTCCATCTCCCTGTCTGTGGAGACAGAGTCACCACTACT 66
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20

Db 1 GluLeuThrGlnSerProSerSerLeuSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGACAAAGTCAAGCAATTAGCAGCTAATTAATTTGGTATCAGACAGAAACAGAGACAG 126
Db 21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnProGlyLys 40
QY 127 CCTCCCAAGCTCTGCTCATTTACTGTGGCATTAACCGGAATCCGGGTCCTGACGATTC 186
Db 41 AlaProLysLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
QY 187 AGTGGACGCGGCTGTGGAGAGATTTCATCTCCATCCAGATCTACAACTTGAAGT 246
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnPhe 80
QY 247 TCTGCACTTACTACTGTGACAGAGATTACGATCCCGTACACTTTGGCCAGGGGACC 306
Db 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnThr 100
QY 307 AAGCTGGAGATCAA 321
Db 101 LysLeuGluIleLys 105

RESULT 8

US-10-727-155-308
; Sequence 308, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Vaspel S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-308

Alignment Scores:
Pred. No.: 4.1e-40 Length: 107
Score: 465.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.44% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x US-10-727-155-308 (1-107)

QY 1 GAGCTCCAGATGACCAAGTCTCCATCTCCCTGTCTGTGGAGACAGAGTCACCACTACC 60
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
QY 61 ATCACTTGTGGCAAGTTCAGACATTAGCAGCTAATTAATGATATCAGCAGAAACA 120


```

1 FILE REFERENCE: 8039/2032
2 CURRENT APPLICATION NUMBER: US/10/409,814A
3 CURRENT FILING DATE: 2003-04-09
4 NUMBER OF SEQ ID NOS: 42
5 SOFTWARE: PatentIn version 3.1
6 SEQ ID NO 4
7 LENGTH: 108
8 TYPE: PRT
9 ORGANISM: Homo sapiens
10 US-10-409-814A-4

Alignment Scores:
Pred. No.: 5,23e-40 Length: 108
Score: 464.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.26% Indels: 0
DB: 16 Gaps: 0

US-09-403-107-141 (1-321) x US-10-409-814A-4 (1-108)

QY 1 GAGCTCCAGATGACCCAGAGCTCCATCTCCCTGCTTCTGCGGAGACAGAGTCACC 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ASpIIGlMeIhtrInserProSerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 61 ATCACTTGTGCGACAGTGCAGACATTAGCAGACTTAAATGGTATCAGCAAAACA 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 IItHhCYaIrGAlaSerGInserIleSerSerTyrlLeuAenITpTyrgInGInLysPro 40

QY 121 GAGACGCTCTTAAAGCTGCTCATTTAGCGATTCACCCGGAATCCGGGGTCCCTGAC 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 41 GLylyAlAProLysLeuLeuIleTyrlAlaAlaSerSerLeuGInSerGlyValProSer 60

QY 181 CGATTGAGTGGCGCGGGTCTGGAGACAGATTTCACCTCACCATCAGACGTCACAACT 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ArpHseSerIySerGlySerGlyThrAspPheTrnIleuTrnIleSerSerLeuGInPro 80

QY 241 GAAGATTCTGCACCTACTACTGTCTGCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 GluAspPheAlaIhTrTyrlTyrlCysGInGInSerTyrlSerTrnProAenTrnPheGlyGln 100

QY 301 GGGACCAAGCTGGAGATCAA 321
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 GlyThrLysValGluIleLys 107

RESULT 12
US-10-726-332-28
1 Sequence 28, Application US/10726332
2 Publication No. US20050058649A1
3 GENERAL INFORMATION:
4 APPLICANT: Gregory M. Landes
5 APPLICANT: Mary Haak-Frendescho
6 APPLICANT: Ling Chen
7 APPLICANT: Yen-Wah K. Lee
8 APPLICANT: Meina Liang
9 APPLICANT: Xiao Feng
10 APPLICANT: Xiao-Chi Jia
11 APPLICANT: Mark R. Nocerini
12 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
13 FILE REFERENCE: ABGENIX.072A
14 CURRENT APPLICATION NUMBER: US/10/726,332
15 CURRENT FILING DATE: 2003-12-02
16 PRIOR APPLICATION NUMBER: n/a
17 PRIOR FILING DATE:
18 NUMBER OF SEQ ID NOS: 222
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 28
21 LENGTH: 108
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 US-10-726-332-28

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Alignment Scores:					
Pred. No.:	5,23e-40	Length:	108		
Score:	464.00	Matches:	90		
Percent Similarity:	90.65%	Conservative:	7		
Best Local Similarity:	84.11%	Mismatches:	10		
Query Match:	81.26%	Indels:	0		
DB:	17	Gaps:	0		
US-09-403-107-141 (1-321) x US-10-726-332-28 (1-108)					
QY	1	GAGCTCAATGATACCCAGTCTTCATCCTCGTGCTGTCTGTGGAGACAAGTACC	60		
Db	1	AspIleGImerThcInSerProSeerSeurLeuSerAlaSerValGlYaPaPqValThr	20		
QY	61	ATACACTTGCGACAAAGTCAGACATTGACGACTTTAAATGGATTCAGCAAACA	120		
Db	21	IleThcCyArGlAlaSerClnSerIlleSeerSerTyRleuMaTrIPtyrGlnGlnHyPro	40		
QY	121	GAGACAGCTCTTAAGTGTCTATTATTCGGAGCTACCCGGGAATCCGGGGTCCCTGAC	180		
Db	41	GLyVaAlaProLySeuLeuIlleTyrlAlaIaSeSerIeuGlnSerGlyValProSer	60		
QY	181	CGATTTAGTGGCAGCGGGTCTGGGACAATTTCACTCTCACCATCAGCAAGTTCACAACT	240		
Db	61	AArgPeSeGeLySerClYserClYthrAapPhetThrLeuthrIlleSaerSerIeuGlnPro	80		
QY	241	GAGATTTCGCAACTTACTACTGTGAGCAGAGATTACGACATCCCGTACACTTTGGCCAG	300		
Db	81	GIuApSPheAlaThrTyrrTyrcysGlnIuSerTyraenThrProPothrPheGlnHyGln	100		
QY	301	GGGACCAAGCTGGAGATCAA 321			
Db	101	GLYThrLyVaAlGlJuIleLys 107			
RESULT 13					
US-09-192-854-2					
Sequence 2, Application US/09192854					
Patent No. US20020068276A1					
GENERAL INFORMATION:					
APPLICANT: Winter, Greg					
TITLE OF INVENTION: Methods for Selecting Functional Peptides					
FILE REFERENCE: 3789/72916					
CURRENT APPLICATION NUMBER: US/09/192,854					
CURRENT FILING DATE: 1998-11-17					
EARLIER APPLICATION NUMBER: 60/066,729					
EARLIER FILING DATE: 1997-11-21					
NUMBER OF SEQ ID NOS: 212					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 2					
LENGTH: 240					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-192-854-2					
Alignment Scores:					
Pred. No.:	5.78e-40	Length:	240		
Score:	464.00	Matches:	90		
Percent Similarity:	89.72%	Conservative:	6		
Best Local Similarity:	84.11%	Mismatches:	11		
Query Match:	81.26%	Indels:	0		
DB:	9	Gaps:	0		
US-09-403-107-141 (1-321) x US-09-192-854-2 (1-240)					
QY	1	GAGCTCAATGATACCCAGTCTTCATCCTCGTGCTGTGGAGACAAGTACC	60		
Db	133	AspIleGImerThcInSerProSeerSeurLeuSerAlaSerValGlYaPaPqValThr	152		
QY	61	ATACACTTGCGACAAAGTCAGACATTGACGACTTTAAATGGATTCAGCAAACA	120		
Db	153	IleThcCyArGlAlaSerClnSerIlleSeerSerTyRleuMaTrIPtyrGlnGlnHyPro	172		

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QY 122 GGACGACCTCCCTAAGCGCTCATTTACTTGGGAGATCCCGGAAATCCGGGGTCCCTGAC 180
Db 173 GilyrsAlProlylsneuulIeTyrlAlAlaserIeuInserGlyValProSer 192
QY 181 CGATTTCAGTGGACCGGGTCTGGGACAGATTTCACTCTCAACATCAGACAGCTCAACT 240
Db 193 ArgpHeSerGlyserGlyserGlyThrAspPhehrIeuhrIeSerSerIeuGlnPro 212
QY 241 GAAGATTTGGCAACTTACTACTGTCAAGACAGATTACGACATCCCGTACACTTTTGGCCAG 300
Db 213 GluAspPheAlaThrTyTCysGlnGlnIserTySerThrProAnthrPheGlyGln 232
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 233 GlyThrLysValGlnIleIlys 239

RESULT 14
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-968-561A-2

Alignment Scores:
Pred. No.: 5,78e-40 Length: 240
Score: 464.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.26% Indels: 0
DB: 9 Gaps: 0

US-09-403-107-141 (1-321) x US-09-968-561A-2 (1-240)
QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTCACC 60
Db 133 AapIleGlnMerThrGlnSerProSerSerIeuSerAlaSerValGlyAspArgValThr 152
QY 61 ATCACTTGGCGGACAGTCAAGACATTTAGACGCTATTAAATGGTATTCAGCAAGAAACCA 120
Db 153 IleThrCysArgAlaSerGlnSerIleSerSerTyIleuAnthrTyrlGlnGlnLysPro 172
QY 121 GGACAGCCCTCTPAAGCTGCTCATTTACTGTGCGCATCTCCCGGAAATCCGGGGTCCCGAC 180
Db 173 GilyrsAlProlylsneuulIeTyrlAlAlaserIeuGlnSerGlyValProSer 192
QY 181 CGATTTCAGTGGACCGGGTCTGGGACAGATTTCACTCTCAACATCAGACAGCTCAACT 240
Db 193 ArgpHeSerGlyserGlyserGlyThrAspPhehrIeuhrIeSerSerIeuGlnPro 212
QY 241 GAAGATTTGGCAACTTACTACTGTCAAGACAGATTACGACATCCCGTACACTTTTGGCCAG 300
Db 213 GluAspPheAlaThrTyTCysGlnGlnIserTySerThrProAnthrPheGlyGln 232

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Db      213 GluAephnealThrTyrrCysGInInsertYserThrProAntnrPhcGlyGln 232
QY      301 GGGACCAAGCTGGAGATCAAA 321
      |||:::|||||
Db      233 GlyThrIysValGlnIleLys 239

RESULT 15
US-09-968-744A-2
/ Sequence 2, Application US/09968744A
/ Publication No. US20030148372A1
/ GENERAL INFORMATION:
/ APPLICANT: Tomlinson, Ian M
/ APPLICANT: Winter, Gregory
/ TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
/ FILE REFERENCE: 8039/1073
/ CURRENT APPLICATION NUMBER: US/09/968,744A
/ PRIORITY FILING DATE: 2003-01-13
/ PRIOR APPLICATION NUMBER: GB 9722131.1
/ PRIOR FILING DATE: 1997-10-20
/ PRIOR APPLICATION NUMBER: US 60/065,248
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: US 60/066,729
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: PCT/GB98/03135
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: US 09/511,939
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-968-744A-2

Alignment Scores:
Pred. No.: 5 78e-40 Length: 240
Score: 464.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.26% Indels: 0
DB: 10 Gaps: 0

US-09-403-107-141 (1-321) x US-09-968-744A-2 (1-240)
QY      1 GAGTCACGATGACCCAGCTCCATCTCCCTGTCGTTCTGGGAGACAGAGTCACC 60
      :::::|||||
Db      133 AepIleGInMeThrGInserProSerSerIleSerValGlyAephValThr 152
      |||:::|||||
QY      61 ATCACTTGTGGACAAAGTCAGAGCATTTACGAGCTATTAATTTGATTCAGAGAAACA 120
      |||:::|||||
Db      153 IleThrYsArgAlaSerGInserIleSerSerTyLeuAntnrPhyGInGlnIlyPro 172
      |||:::|||||
QY      121 GGACGAGCTCCCTTAAGCTGTCTATTACTGGCATCTACCCGGGAATCCGGGTCCTTGAC 180
      |||:::|||||
Db      173 GlyIysAlaProIlyLeuMetIleTyrrAlaAlaSerSerIleuInserGlyValProSer 192
      |||:::|||||
QY      181 CGATTACAGTGGAGCGGGCTGTGGACAGATTTCACTTCACCTACGACAGCTTACAACT 240
      |||:::|||||
Db      193 ArgPheSerGlySerGlySerAllyThrAephneThrIleSerSerIleuGInPro 212
      |||:::|||||
QY      241 GAAGATTCTGCAACTTACTACTGTCTACGACAGAGTTACAGACATCCCGTACACTTTGGCCAG 300
      |||:::|||||
Db      213 GluAephnealThrTyrrCysGInGInserTySerThrProAntnrPhcGlyGln 232
      |||:::|||||
QY      301 GGGACCAAGCTGGAGATCAAA 321
      |||:::|||||
Db      233 GlyThrIysValGlnIleLys 239
      |||:::|||||

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Job time : 302.423 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 14.4038 Seconds
(without alignments)
4288.519 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCLALIGN=200 -THR.SCORB=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09403107@cgn.1.1.77@runat.29082005.120125.18902 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG.SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV.TIMEOUT=130 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	81.3	123	2	S40331
2	463	81.1	109	2	S31981
3	462	80.9	127	2	S40367
4	460	80.6	109	2	S31998
5	458	80.2	108	2	B49047
6	451	79.0	108	2	S47182
7	450	78.8	129	1	KIHUWK
8	449	78.5	109	2	S31978
9	448	78.5	129	2	S52792
10	446	78.1	108	2	S44122
11	445	77.9	109	2	S31979
12	441	77.2	108	2	S19674
13	441	77.2	109	2	S31980
14	438	76.7	120	2	S46370

15	437	76.5	108	2	S31977	Ig kappa chain - h
16	437	76.5	117	2	S46371	Ig kappa chain V-J
17	436	76.4	108	1	KIHUHW	Ig kappa chain V-I
18	436	76.4	129	2	S40317	Ig kappa chain - h
19	435	76.2	109	2	S31983	Ig kappa chain - h
20	435	76.2	114	1	K4HULN	Ig kappa chain V-I
21	435	76.2	129	2	S52793	Ig kappa chain V r
22	434	76.0	107	2	S36264	Ig lambda chain V
23	433.5	75.9	125	2	S40315	Ig kappa chain - h
24	433	75.8	108	1	KIHULY	Ig kappa chain V-I
25	433	75.8	125	2	S40333	Ig kappa chain V-J
26	432.5	75.7	107	2	S36275	Ig lambda chain V
27	432	75.7	109	2	S32001	Ig kappa chain - h
28	432	75.7	125	2	S40350	Ig kappa chain - h
29	428	75.0	107	2	S36268	Ig lambda chain V
30	428	75.0	122	2	S40370	Ig kappa chain - h
31	428	75.0	131	2	S40352	Ig kappa chain V-J
32	425	74.4	113	2	S34002	Ig kappa chain V r
33	424	74.3	108	1	KIHUDE	Ig kappa chain V-I
34	424	74.3	126	2	S40335	Ig kappa chain V-J
35	423	74.1	128	2	S46372	Ig light chain var
36	422.5	74.0	108	2	S30521	Ig kappa chain V r
37	422	73.9	107	2	S36269	Ig lambda chain V
38	422	73.9	108	1	KIHURE	Ig kappa chain V-I
39	422	73.9	108	2	I39154	Ig kappa chain (BR
40	422	73.9	129	2	S52789	Ig kappa chain V r
41	422	73.9	134	1	K4HUI7	Ig kappa chain pre
42	421	73.7	108	1	KIHUUV	Ig kappa chain V-I
43	421	73.7	120	2	S51147	antibody light cha
44	420	73.6	108	1	KIHOUU	Ig kappa chain V-I
45	420	73.6	129	2	S40369	Ig kappa chain - h

ALIGNMENTS

RESULT 1
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLB>
A/Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 2.41e-34
Score: 464.00
Percent Similarity: 89.72%
Best Local Similarity: 84.11%
Query Match: 81.26%
DB: 2
Gaps: 0

US-09-403-107-141 (1-321) x S40331 (1-123)

QY	1	GAGCTCCAGATGACCCAGCTCCATCTCCCTGCTGCTTCTGTGGAGACAGATCACC	60
DB	17	AspIeGlnMetThrGlnSerProSerSerLeuSerLaserValGlyAspArgValThr	36
QY	61	ATCACTTGTGGACAGACTGACAGCATTAAAGCATTTAATGGATTCGCGAAACCA	120
DB	37	IleThrCysArgAlaSerGlnSerIleSerSerTyrluAsnTrpYrGlnGlnIuYpPro	56
QY	121	GGAGAGCTCTTAAGCTGCTCATTTACTGCGGATCTTACCGGGAATCCGGGGTCCCTGAC	180

```

Db      57  GILYVSLAProlylsLeuIleTyrAlaLaserSerLeuGlnSerGlyValProSer 76
QY      181  CGATTGAGTGGACGGGCTCGGACAGATTTCATCTCCATCAGACAGTTCACACT 240
Db      77  ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 96
QY      241  GAAGATTCTGCACACTTACTACTGTGCAGACAGATTACACATCCCGTACACTTTTGGCCAG 300
Db      97  GlnAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProArgThrPheGlyGln 116
QY      301  GGGACCAAGCTGGAGATCAAA 321
Db      117  GlyThrIysValGluIleIys 123

```

RESULT 2

```

S31981
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31981
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:G38494
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:

```

Pred. No.:      3.01e-34      Length:      109
Score:          463.00      Matches:      91
Percent Similarity: 87.85%      Conservative: 3
Best Local Similarity: 85.05%      Mismatches: 13
Query Match:    81.09%      Indels:      0
Gaps:           2           Gaps:         0

```

US-09-403-107-141 (1-321) x S31981 (1-109)

```

QY      1  GAGCTCCAGATGACCCGATCTCCATCCTGCTGCTTCTGTGGAGACAGATCAC 60
Db      1  GILYVSLAProlylsLeuIleTyrAlaLaserSerLeuGlnSerGlyValProSer 20
QY      61  ATCACTTGTGGACAGATGACGAGCATTAGAGCATTAATTAATTGGTATCAGAGAAACA 120
Db      21  ILeThrCysArgAlaSerGlnAspPheIleSerThrGlyLeuAsnThrPyrGlnGlnIysPro 40
QY      121  GAGACAGCTCTTAAGCTGCTCATTTACTTGGGATTCACCGGGAATCCGGGGTCCCTGAC 180
Db      41  GILYVSLAProlylsLeuIleIleHISGLYAlaSerThrIleuGlnSerGlyValProGly 60
QY      181  CGATTGAGTGGACGGGCTCGGACAGATTTCATCTCCATCAGACAGTTCACACT 240
Db      61  ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 80
QY      241  GAAGATTCTGCACACTTACTACTGTGCAGACAGATTACACATCCCGTACACTTTTGGCCAG 300
Db      81  GlnAspPyrAlaThrTyrTyrCysGlnGlnSerTyrSerThrProPheThrPheGlyGln 100
QY      301  GGGACCAAGCTGGAGATCAAA 321
Db      101  GlyThrIysLeuGluIleIys 107

```

RESULT 3

```

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

```

```

C/Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:

```

Pred. No.:      3.64e-34      Length:      127
Score:          462.00      Matches:      88
Percent Similarity: 91.59%      Conservative: 10
Best Local Similarity: 82.24%      Mismatches: 9
Query Match:    80.91%      Indels:      0
Gaps:           2           Gaps:         0

```

US-09-403-107-141 (1-321) x S40367 (1-127)

```

QY      1  GAGCTCCAGATGACCCGATCTCCATCCTGCTGCTTCTGTGGAGACAGATCAC 60
Db      18  AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 37
QY      61  ATCACTTGTGGACAGATGACGAGCATTAATTAATTGGTATCAGAGAAACA 120
Db      38  ILeThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnThrTyrGlnIArgIysPro 57
QY      121  GAGACAGCTCTTAAGCTGCTCATTTACTTGGGATTCACCGGGAATCCGGGGTCCCTGAC 180
Db      58  GILYVSLAProlylsLeuIleTyrAlaLaserSerLeuGlnSerGlyValProSer 77
QY      181  CGATTGAGTGGACGGGCTCGGACAGATTTCATCTCCATCAGACAGTTCACACT 240
Db      78  ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 97
QY      241  GAAGATTCTGCACACTTACTACTGTGCAGACAGATTACACATCCCGTACACTTTTGGCCAG 300
Db      98  GlnAspPheAlaThrTyrTyrCysGlnGlnSerTyrAsnThrProThrPheGlyGln 117
QY      301  GGGACCAAGCTGGAGATCAAA 321
Db      118  GlyThrIysValGluIleIys 124

```

RESULT 4

S31998

```

Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:

```

Pred. No.:      5.64e-34      Length:      109
Score:          460.00      Matches:      89
Percent Similarity: 89.72%      Conservative: 7
Best Local Similarity: 83.18%      Mismatches: 11
Query Match:    80.56%      Indels:      0

```


DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x S31998 (1-109)

QY 1 GAGCTCCAGATGACCCAGCTTCATCTCCCTGCTGCTTGTGGAGACAGAGTCAAC 60
| | | | |
Db 1 GlutLeuValMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
| | | | |
QY 61 ATCACTGTGGACAGATGACAGCATTTAGACGCTTTAAATGGTATACAGCAAAACA 120
| | | | |
Db 21 IleThrCysArgAlaSerGlnSerIleSerValTyrLeuAsnTrpTyrGlnIleLysPro 40
| | | | |
QY 121 GGACAGCCTCTCAAGCTGCTCATTTACTGCGCATCCCGGAGATCCGGGTCCTGAC 180
| | | | |
Db 41 GlyValAlaProLysLeuLeuIleTyrSerAlaSerLeuGlnSerGlyValProSer 60
| | | | |
QY 181 CGATTCACTGGACAGCGGCTCTGGAGACAGATTTCATCTCACCATCAGACGCTCAACCT 240
| | | | |
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
| | | | |
QY 241 GAAGATTCTGCACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTTGGCCAG 300
| | | | |
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrAspThrProTrpThrPheGlyHis 100
| | | | |
QY 301 GGAGCAAGCTGGAGATCAAA 321
| | | | |
Db 101 GlyThrLysValGluIleLys 107
| | | | |

RESULT 5

B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:151616
A:Accession: B49047
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes (NCBI:113208, NCBI:P:113209)
A:Note: Sequence extracted from NCBI Backbone
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:16-90/Domain: Immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	8.58e-34	Length:	108
Score:	458.00	Matches:	89
Percent Similarity:	88.79%	Conservative:	6
Best Local Similarity:	83.18%	Mismatches:	12
Query Match:	80.21%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x B49047 (1-108)

QY 1 GAGCTCCAGATGACCCAGCTTCATCTCCCTGCTGCTTGTGGAGACAGAGTCAAC 60
| | | | |
Db 1 AsplIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
| | | | |
QY 61 ATCACTGTGGACAGATGACAGCATTTAGACGCTTTAAATGGTATACAGCAAAACA 120
| | | | |
Db 21 IleThrCysArgAlaSerGlnSerIleSerValTyrLeuAsnTrpTyrGlnIleLysPro 40
| | | | |
QY 121 GGACAGCCTCTCAAGCTGCTCATTTACTGCGCATCCCGGAGATCCGGGTCCTGAC 180
| | | | |
Db 41 GlyValAlaProLysLeuLeuIleTyrAlaAlaSerLeuGlnSerGlyValProSer 60
| | | | |
QY 181 CGATTCACTGGACAGCGGCTCTGGAGACAGATTTCATCTCACCATCAGACGCTCAACCT 240
| | | | |
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
| | | | |

QY 241 GAAGATTCTGCACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTTGGCCAG 300
| | | | |
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProLeuThrPheGlyGly 100
| | | | |
QY 301 GGAGCAAGCTGGAGATCAAA 321
| | | | |
Db 101 GlyThrLysValGluIleLys 107
| | | | |

RESULT 6

S47182
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47182
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A:Reference number: S47181
A:Accession: S47182
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MC1>
A:Cross-references: EMBL:X79786; NID:9506422; PIDN:CAA56182.1; PID:9506423
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: Immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	3.71e-33	Length:	108
Score:	451.00	Matches:	88
Percent Similarity:	87.85%	Conservative:	6
Best Local Similarity:	82.24%	Mismatches:	13
Query Match:	78.98%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S47182 (1-108)

QY 1 GAGCTCCAGATGACCCAGCTTCATCTCCCTGCTGCTTGTGGAGACAGAGTCAAC 60
| | | | |
Db 1 GluThrLysLeuThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
| | | | |
QY 61 ATCACTGTGGACAGAACTGACAGATTAAGCATTAATTAATGGTATACAGCAAAACA 120
| | | | |
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnIleLysPro 40
| | | | |
QY 121 GGACAGCCTCTCAAGCTGCTCATTTACTGCGCATCCCGGAGATCCGGGTCCTGAC 180
| | | | |
Db 41 GlyValAlaProLysLeuLeuIleTyrAlaAlaSerLeuGlnSerGlyValProSer 60
| | | | |
QY 181 CGATTCACTGGACAGCGGCTCTGGAGACAGATTTCATCTCACCATCAGACGCTCAACCT 240
| | | | |
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
| | | | |
QY 241 GAAGATTCTGCACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTTGGCCAG 300
| | | | |
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProLeuThrSerGlyGln 100
| | | | |
QY 301 GGAGCAAGCTGGAGATCAAA 321
| | | | |
Db 101 GlyThrArgLeuGluIleLys 107
| | | | |

RESULT 7

K1H0WK
Ig kappa chain precursor V-I region (Walker) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01883
R:Klobeck, H.G.; Combrilato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A:Reference number: A93534; MUID:85014148; PMID:6091049
A:Accession: A01883

A:Molecule type: DNA
 A:Residues: 1-129 <KLO>
 A/Cross-references: UNIPROT:P04431
 A/Note: the sequence was determined from the differentiated gene
 C/Genetics:
 A:Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/product: Ig kappa chain V-I region (Walker) #status predicted <MT>
 F:23-45/Region: framework 1
 F:38-112/Domain: immunoglobulin homology <IMM>
 F:46-56/Region: complementarity-determining 1
 F:57-71/Region: framework 2
 F:72-78/Region: complementarity-determining 2
 F:79-110/Region: framework 3
 F:111-119/Region: complementarity-determining 3
 F:120-129/Region: framework 4
 F:45-110/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.:	4,46e-33	Length:	129
Score:	450.00	Matches:	88
Percent Similarity:	88.79%	Conservative:	7
Best Local Similarity:	82.24%	Mismatches:	12
Query Match:	78.81%	Indels:	0
DB:	1	Gaps:	0

US-09-403-107-141 (1-321) x KIHUMK (1-129)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGATCACC 60
 : : : : :
 Db 23 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 42

QY 61 ATCACTTGTGGACAAGTCAGATGAGATTAAGCAATTAATGGTTTCAGCAAAACCA 120
 : : : : :
 Db 43 IleThrCysArgAlaSerGlnSerIleSerAsnIleuSerTrpYrGlnGlnLeuPro 62

QY 121 GACAGCCTCTAAGTGTCTCATTTACTGCGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
 : : : : :
 Db 63 GlyIleValaProIysLeuIleIleTyrAlaAlaSerSerIleuGlnSerGlyValThrSer 82

QY 181 CGATTCAGTGGACGGGGTCTGGACAGATTTCATCTCCATCCATCAGCAGTTCACACT 240
 : : : : :
 Db 83 ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 102

QY 241 GAAGATTCTGCACCTTACTCTGTCGACAGAGTTACACATCCCGTACATTTTGGCCAG 300
 : : : : :
 Db 103 GluAspSerAlaThrIleTyrIleCysGlnGlnIleSerIleThrIleuIleThrPheGlyGln 122

QY 301 GGGACCAAGCTGGAGATCAAA 321
 : : : : :
 Db 123 GlyThrArgLeuGlnIleIys 129

RESULT 8
 S31978
 Ig kappa chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S31978
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A/Reference number: S31977
 A/Accession: S31978
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-109 <PDR>
 A/Cross-references: EMBL:Z15074; NID:g38487; PIDN:CAA78783.1; PID:g38488

C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	5.62e-33	Length:	109
Score:	449.00	Matches:	87
Percent Similarity:	87.85%	Conservative:	7
Best Local Similarity:	81.31%	Mismatches:	13
Query Match:	78.63%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S31978 (1-109)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGATCACC 60
 : : : : :
 Db 1 GluLeuValMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 61 ATCACTTGTGGACAAGTCAGATGAGATTAAGCAATTAATGGTTTCAGCAAAACCA 120
 : : : : :
 Db 21 IleThrCysArgThrSerGlnThrIleSerArgIleuAsnTrpIleGlnIlePro 40

QY 121 GACAGCCTCTAAGTGTCTCATTTACTGCGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
 : : : : :
 Db 41 GlyIleValaProIysLeuIleIlePheAlaIleSerThrLeuGlnThrGlyValProSer 60

QY 181 CGATTCAGTGGACGGGGTCTGGACAGATTTCACCTTCATCCATCAGCAGTTCACACT 240
 : : : : :
 Db 61 ArgPheGlyIleSerIleSerGlyThrAspPheThrIleuThrIleSerThrLeuGlnPro 80

QY 241 GAAGATTCTGCACCTTACTCTGTCGACAGATTTCACATCCCGTACATTTTGGCCAG 300
 : : : : :
 Db 81 AspAspPheAlaThrIleTyrIleCysGlnGlnIleSerIleThrIleProIleThrPheGlyGln 100

QY 301 GGGACCAAGCTGGAGATCAAA 321
 : : : : :
 Db 101 GlyThrArgLeuGlnIleIys 107

RESULT 9
 S52792
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 C/Accession: S52792
 R/Bocsi, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoy, L.; Deret,
 submitted to the EMBL Data Library, March 1995
 A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-
 A/Reference number: S52789
 A/Accession: S52792
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-129 <ROC>
 A/Cross-references: EMBL:X85996; NID:g758598; PIDN:CAA5988.1; PID:g758599
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:38-112/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	6.78e-33	Length:	129
Score:	448.00	Matches:	85
Percent Similarity:	87.85%	Conservative:	9
Best Local Similarity:	79.44%	Mismatches:	13
Query Match:	78.46%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S52792 (1-129)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGATCACC 60
 : : : : :
 Db 23 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 42

QY 61 ATCACTTGTGGACAAGTCAGATGAGATTAAGCAATTAATGGTTTCAGCAAAACCA 120
 : : : : :
 Db 101 GlyThrArgLeuGlnIleIys 107

Db 43 IleThrCysArgAlaSerGlnSerIleAlaGlyTyrLeuAenTrpTyrGlnGlnArgPro 62
Qy 121 GGACGCTCCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCCCTGAC 180
Db 63 GlyValAlaProGlnLeuLeuIleTyrAlaAlaSerThrLeuArgSerGlyValProSer 82
Qy 181 CGATTCAGTGGAGGGGCTGGGACAGATTTCATCTCACACATGAGAGAGTCTAAACCT 240
Db 83 ArgPheSerGlySerGlySerGlyValAlaPheThrLeuThrIleSerSerLeuGlnPro 102
Qy 241 GAAGATTCTGCAACTTACTACTGTGAGCAGATTACGATCCGCTACACTTTTGCCAG 300
Db 103 GluAlaSerAlaIleThrTyrCysGlnGlnInsertyrGlyThrProPheThrPheGlyPro 122
Qy 301 GGGACCAAGCTGGAGATCAA 321
Db 123 GlyThrLysValAlaPheIleLys 129

RESULT 10

S44122
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44122
R:Hawkins, R.E.; Zhu, D.; Owecke, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44122
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <HAW>
A/Cross-references: EMBL:Z31390, NID:9472976, PIDN:CAA93265.1, PID:9340533
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,05e-32 Length: 108
Score: 446.00 Matches: 87
Percent Similarity: 87.85% Conservative: 7
Best Local Similarity: 81.31% Mismatches: 13
Query Match: 78.11% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x S44122 (1-108)

Qy 1 GAGCTCAGATGACCCAGCTCCATCTCCCTGCTGCTGCTGGAGAGAGTCAAC 60
Db 1 AsplIeGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
Qy 61 ATCACTTGTGGACAAAGTCAGACATTAGACGATTAATAATTGGTATCAGCAAAACA 120
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAenTrpTyrGlnGlnLysLeu 40
Qy 121 CGACAGCTCCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCCCTGAC 180
Db 41 GlyValAlaProGlnLeuLeuIleTyrSerAlaSerSerLeuGlnSerGlyValProSer 60
Qy 181 CGATTCAGTGGAGGGGCTGGGACAGATTTCATCTCACACATGAGAGAGTCTAAACCT 240
Db 61 ThrPheSerGlySerGlySerGlyValAlaPheThrLeuThrIleSerSerLeuGlnPro 80
Qy 241 GAAGATTCTGCAACTTACTACTGTGAGCAGATTACGATCCGCTACACTTTTGCCAG 300
Db 81 GluAlaSerAlaIleThrTyrCysGlnGlnInsertyrSerThrProTrpThrPheGlyPro 100
Qy 301 GGGACCAAGCTGGAGATCAA 321
Db 101 GlyThrLysValAlaPheIleLys 107

RESULT 11

S31979

Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31979
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; Mclachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31979
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15075, NID:938489, PIDN:CAA78784.1, PID:938490
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.3e-32 Length: 109
Score: 445.00 Matches: 86
Percent Similarity: 86.92% Conservative: 7
Best Local Similarity: 80.37% Mismatches: 14
Query Match: 77.93% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x S31979 (1-109)

Qy 1 GAGCTCAGATGACCCAGCTCCATCTCCCTGCTGCTGCTGGAGAGAGTCAAC 60
Db 1 GluLeuValMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
Qy 61 ATCACTTGTGGACAAAGTCAGACATTAGACGATTAATAATTGGTATCAGCAAAACA 120
Db 21 IleSerCysArgAlaSerGlnSerIleGlyLysTyrLeuAenTrpTyrArgGlnLysPro 40
Qy 121 GGAAGCTCCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCCCTGAC 180
Db 41 GlyValAlaProGlnLeuLeuIleTyrGlyThrSerThrLeuGlnSerGlyValProSer 60
Qy 181 CGATTCAGTGGAGGGGCTGGGACAGATTTCATCTCACACATGAGAGAGTCTAAACCT 240
Db 61 ArgPheSerGlySerGlyPheGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
Qy 241 GAAGATTCTGCAACTTACTACTGTGAGCAGATTACGATTCACCAATCCGCTACACTTTTGCCAG 300
Db 81 GluAlaSerAlaIleThrTyrPheCysGlnGlnInsertyrSerSerProTyrThrPheGlyPro 100
Qy 301 GGGACCAAGCTGGAGATCAA 321
Db 101 GlyThrLysValAlaPheIleLys 107

RESULT 12

S19674
Ig kappa chain V region (clone alpha-TEU) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19674
J:Mark, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.M.; B101. 222, 581-597, 1991
A/Title: BV-passing immunization. Human antibodies from V-gene libraries displayed on phage
A/Reference number: S19663; PMID:92085276; PMID:11748994
A/Accession: S19674
A/Molecule type: mRNA
A/Residues: 1-108 <MAR>
A/Cross-references: EMBL:X61642, NID:937860, PIDN:CAA43823.1, PID:91335386
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 3e-32 Length: 108
Score: 441.00 Matches: 86
Percent Similarity: 86.92% Conservative: 7

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <PQR>
A:Cross-references: UNIPROT:Q96SA9; EMBL:Z15073
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	6,92e-32	Length:	108
Score:	437.00	Matches:	87
Percent Similarity:	86.92%	Conservative:	6
Best Local Similarity:	81.31%	Mismatches:	14
Query Match:	76.53%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S31977 (1-108)

```
OY      1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGTGGAGACAGAGTCACC 60
        |||||
DB      1 GluLeuValMetThrGlnSerGlySerSerLeuSerAlaSerValGlyAspArgValThr 20
OY      61 ATCACTTGTCCGACAGTCAAGTCAGACATTAAGCACTTAATGGTATCAGCAGAAACCA 120
        |||||
DB      21 IleThrCysArgAlaSerGlnSerIleSerAlaTyrLeuAsnTrpTyrGlnIlyAspPro 40
OY      121 GGACAGCCTCCTTACCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
        |||||
DB      41 GlyIysAlaProLyLeuLeuIleTyrSerAlaSerSerLeuGlnSerGlyValProSer 60
OY      181 CGATTCAAGTGGCAGGGGCTTGGACAGATTCACTTCACCATCAGCAGAGTCTACAACCT 240
        |||||
DB      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
OY      241 GAAGATTCTGCAACTTACTACTGTCTGACAGAGTTAGACATCCCGTACACTTTGGCCAG 300
        |||||
DB      81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrAspThrValAspThrPheGlyHis 100
OY      301 GGGACCAAGCTGGAGATCAA 321
        |||||
DB      101 GlyThrIysValGluIleLys 107
```

Search completed: August 29, 2005, 11:31:14
Job time : 16.4038 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 68.3611 Seconds
(without alignments)
4809.091 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571
Sequence: 1 gagctccagatgaccagtc.....ggaccaagctggagatcaaa 321

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p_model -DEV=xlp
-O=/cgn2_1/USPTO_epool_p/US09403107/runat_29082005_120124_18889/app_query.fasta_1.1038
-DB=uniprot -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09403107@cgn_1_1_305@runat_29082005_120124_18889 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	79.2	108	Q9UL77	Q9UL77 homo sapien
2	450	78.8	129	KV1M_HUMAN	P0431 homo sapien
3	440.5	77.1	107	Q96SA9	Q96SA9 homo sapien
4	436	76.4	108	KV1J_HUMAN	P01600 homo sapien
5	435	76.2	134	KV4C_HUMAN	P06314 homo sapien
6	434	76.0	114	KV4A_HUMAN	P01625 homo sapien
7	433	75.8	108	KV1M_HUMAN	P01605 homo sapien
8	433	75.8	236	O6GMW1	O6GMW1 homo sapien
9	433	75.8	236	O6GMX8	O6GMX8 homo sapien
10	431	75.5	108	KV1E_HUMAN	P01597 homo sapien
11	424	74.3	108	Q9UL70	Q9UL70 homo sapien
12	424	74.3	108	KV1O_HUMAN	P01607 homo sapien
13	422	73.9	108	KV1J_HUMAN	P01594 homo sapien
14	421	73.7	108	KV1N_HUMAN	P01606 homo sapien
15	420	73.6	108	KV1Y_HUMAN	P00362 homo sapien
16	420	73.6	108	KV1Y_HUMAN	P00362 homo sapien

17	420	73.6	236	2	O6P1T5	O6P1T5 homo sapien
18	415.5	72.8	107	2	Q9UL81	Q9UL81 homo sapien
19	414	72.5	236	2	O6P1H7	O6P1H7 homo sapien
20	413	72.3	108	1	KV1V_HUMAN	P04430 homo sapien
21	412	72.2	108	1	KV1K_HUMAN	P01603 homo sapien
22	412	72.2	234	2	Q7Z473	Q7Z473 homo sapien
23	412	72.2	236	2	O7Z3Y4	O7Z3Y4 homo sapien
24	411	72.0	108	1	KV1P_HUMAN	P01608 homo sapien
25	411	72.0	108	2	Q9UL79	Q9UL79 homo sapien
26	407	71.3	108	1	KV1Q_HUMAN	P01604 homo sapien
27	406	71.1	108	1	KV1L_HUMAN	P01604 homo sapien
28	405.5	71.0	133	1	KV4B_HUMAN	P06313 homo sapien
29	404	70.8	108	1	KV1A_HUMAN	P01593 homo sapien
30	404	70.8	108	1	KV1S_HUMAN	P01611 homo sapien
31	403.5	70.7	107	1	KV1D_HUMAN	P01596 homo sapien
32	402	70.4	108	1	KV1C_HUMAN	P01595 homo sapien
33	401	70.2	108	1	KV1R_HUMAN	P01610 homo sapien
34	401	70.2	108	1	KV1P_MOUSE	P01649 mus musculus
35	398	69.7	244	2	O6S2C8	O6S2C8 homo sapien
36	397	69.5	108	1	KV1P_HUMAN	P01598 homo sapien
37	394	69.0	236	2	O6GMX9	O6GMX9 homo sapien
38	394	69.0	240	2	O6S2C9	O6S2C9 homo sapien
39	392	68.7	129	1	KV1X_HUMAN	P04432 homo sapien
40	391.5	68.6	109	1	KV1T_HUMAN	P01612 homo sapien
41	391	68.5	108	1	KV1G_HUMAN	P01599 homo sapien
42	391	68.5	108	1	KV5M_MOUSE	P01646 mus musculus
43	388	68.0	109	1	KV4D_HUMAN	P83593 homo sapien
44	388	68.0	111	2	Q920B9	Q920B9 mus musculus
45	386	67.6	111	1	KV3M_MOUSE	P01665 mus musculus

ALIGNMENTS

RESULT 1
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DS (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; --
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
Alignment Scores:
Pred. No.: 7.19e-40
Score: 452.00
Score: 88.79%
Best Local Similarity: 81.31%
Query Match: 79.16%
Length: 108
Matches: 87
Conservative: 8
Mismatch: 12
Indels: 0
Gaps: 0

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US-09-403-107-141 (1-321) x Q9UL77 (1-108)
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
Db 1 AspIleGImerThrGlnSerProSerSerLeuSerAlaSerValGIYAspArgValThr 20
QY 61 ATCACTTGTGGACAAGTCAGACATTAGACGCTATTAAATTGGTATCGACGAACA 120
Db 21 IIErThrCyArGAlaSerGlnSerIleSerSerThrLeuGlnSerIleGlnGlnSPro 40
QY 121 GACAGCCTCTAGAGTGTCTCATTTACTGCGCATACCCGGGAATCCGGGTCCTGAC 180
Db 41 GILYsAlaProAsnLeuLeuIleTYrAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY 181 CGATTCACTGTGGACGGGGTCTGGACAGATTTCACTTCACCATCAGACGTCACACT 240
Db 61 ArgPheSerGIYserGIYserGIYThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCACACTTACTACTGTCAGACAGATTAGACATCCCGTACACTTTGGCCAG 300
Db 81 GIAspPheAlaThrTYrTYrCYsGlnGlnSerTYrSerThrSerThrPheGlyGlu 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 101 GLYThrIYsValGlnIleIYs 107
RESULT 2
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUMK.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003623; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1Ike.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
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FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISUFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Alignment Scores:
Pred. No.: 129
Score: 1.2e-39 Length: 129
Percent Similarity: 450.00 Matches: 88
Best Local Similarity: 86.79% Conservative: 7
Query Match: 82.24% Mismatches: 12
DB: 78.81% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x KV1W_HUMAN (1-129)
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
Db 23 AspIleGImerThrGlnSerProSerSerLeuSerAlaSerValGIYAspArgValThr 42
QY 61 ATCACTTGTGGACAAGTCAGACATTAGACGCTATTAAATTGGTATCGACGAACA 120
Db 43 IIErThrCyArGAlaSerGlnSerIleSerSerThrLeuGlnSerIleGlnGlnSPro 62
QY 121 GACAGCCTCTAGAGTGTCTCATTTACTGCGCATACCCGGGAATCCGGGTCCTGAC 180
Db 63 GILYsAlaProAsnLeuLeuIleTYrAlaAlaSerSerLeuGlnSerGlyValProSer 82
QY 181 CGATTCACTGTGGACGGGGTCTGGACAGATTTCACTTCACCATCAGACGTCACACT 240
Db 83 ArgPheSerGIYserGIYserGIYThrAspPheThrLeuThrIleSerSerLeuGlnPro 102
QY 241 GAAGATTCTGCACACTTACTACTGTCAGACAGATTAGACATCCCGTACACTTTGGCCAG 300
Db 103 GIAspPheAlaThrTYrTYrCYsGlnGlnSerTYrSerThrSerThrPheGlyGlu 122
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 123 GLYThrArgLeuGlnIleIYs 129
RESULT 3
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.B., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-1Ike.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
```



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DR PROSITE;PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9CSB577F16 CRC64;

Alignment Scores:
Pred. No.: 1,25e-38
Score: 440.50
Percent Similarity: 87.85%
Best Local Similarity: 82.24%
Query Match: 77.15%
DB: 2
Gaps: 1

US-09-403-107-141 (1-321) x Q96SA9 (1-107)
QY 1 GAGCTCCAGATGAGCCAGTCTCCACTCCCTGCTGCTTCTGTGGAGACAGAGTCACC 60
Db 1 AapIleGlnMetThrInserProSerSerLeuSerAlaSerAlaGlyAlaPheGlyThr 20
QY 61 ATCACTTGTTCGGACAAAGTCAGAGCACTTAGCACTTAATAATTGATACGCAAAACA 120
Db 21 IietnCYaIRgAlaSerGlnSerIleSerSerTyLeuAsnTrpYrGlnGlnLyPro 40
QY 121 GGACAGCCCTTCAGAGTGCCTATTACTGCGCATCTACCCGGAATCCGGGGCCCTGAC 180
Db 41 GilyrSaLaProLyLeuLeuIleTyAlaAlaSerSerLeuInserGlyAlaProSer 60
QY 181 CGATTTCAGTGGAGCGCGGTCTGGGACAGATTTCACTCTCAACATCAGACGTCACAACT 240
Db 61 ArgPheSerCylSerCylSerGlyThrAlaPheThrLeuThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCAACTTACTACTGTCTGACAGAGATTGACATCCCGTACACTTTGGCCAG 300
Db 81 GlnaPheAlaThrTyTyTyCysGlnGlnSerTySer---ThrLeuThrPheGlyGly 99
QY 301 GGGACCAAGCTGAGATCAAA 321
Db 100 GilynTrLyLeuAlaGlnIleLyS 106

RESULT 4
KV1L HUMAN
ID KV1L HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hillebreann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1H0HU.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NNS.
DR GO; GO:0003823; P:antigen binding; NNS.
DR GO; GO:0006955; P:immune response; NNS.
DR InterPro; IPR007110; Ig_L-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.

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FT	DOMAIN	1	23	Framework-1.
FT	DOMAIN	24	34	Complementarity-determining-1.
FT	DOMAIN	35	49	Framework-2.
FT	DOMAIN	50	56	Complementarity-determining-2.
FT	DOMAIN	57	88	Framework-3.
FT	DOMAIN	89	97	Complementarity-determining-3.
FT	DOMAIN	98	107	Framework-4.
FT	DISULFID	23	88	By similarity.
FT	NON_TER	108	108	
SEQ	SEQUENCE	108 AA;	11671 MW;	08D3A616DD8D0618 CRC64;

Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:
		3.83e-38	436.00	88.79%	76.36%
				Matches:	108
				Conservative:	84
				Mismatches:	12
				Indels:	0
				Gaps:	0

US-09-403-107-141 (1-321) x KV1H_HUMAN (1-108)
QY 1 GAGCTCCAGATGACCCAGAGTTCATCCCTCGTCTGCTTGTCGGAGACAGAGTACC 60
Db 1 AspliegimetrhnginsePrroserseieuseralaserValGlyAspArgValthr 20
QY 61 ATCACTTGTCGACAGAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAGAAACCA 120
Db 21 IllethrcysAsgalaserGlnserIleaserseYrleuSertrpTyGlnGlnlnysPro 40
QY 121 GGACAGCCTCCTTAAGCTGCTATTACTTGCGGATGATCCCGGAAATCCGGGGTCCCTGAC 180
Db 41 GlylsAlaPProGlnValIleuIleTyrlAlaIaserseIleuProSerGlyValProser 60
QY 181 CGATTTCAGTGCGAGCGGGTCTGGAGACAGATTTCCTCCACATCAGCAGCTTACACT 240
Db 61 ArgpheserGlyserGlyserGlyThrAspphenrleuThrIleSerSerleuGlnPro 80
QY 241 GAAGATTCTCGCAACTTACTACTGTCCAGCAGAGTTACGACATCCGTCACCTTTGGCCAG 300
Db 81 GlusAspphenalThrTrpYrTyCysGlnGlnAsnTrpYrIleThrProThrSerPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 101 GlyThrArgValGluIleIlys 107

RESULT 5
KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappA chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills P., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RL Nucleic Acids Res. 13:6531-6544(1985).
RL [2]
RN REVISION TO 76.
RP Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way


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QY 1 GAGTCCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGCGGAGACAGATCAC 60
Db 1 AspllevalmetrthginserserprospserleuAlaValserleuGIuValgAlaThr 20
QY 61 ATCACTTGTCAGACAGTACGAGCAT-----AGCAGCTATTAAAT 102
Db 21 IleancyslyserSerSerInserValleuTyrserserAsnSerIysAsnTyrlenula 40
QY 103 TGGTATCAGACAGAAACAGAGACAGCTCTTAAGCTGCTCATTTACTGGCGATCAACCGG 162
Db 41 TPTyrgInglInlyProIyglInProIySleuLeuIleTyrtPAlaserThrArg 60
QY 163 GAATCCGGGGTCCCTGACCGGATTCAGTGGCAGCGGGTCTGGACAGATTTCAGTCCACC 222
Db 61 GluserglyValProAspArgPheSerGlySerGlyThrAspPheThrLeuThr 80
QY 223 ATCAGCAGTCTCAACCTGAGAGATTCGCACTTACTACTGTCTCAGCAGAGTTCAGACATC 282
Db 81 IleserSerleuGlnAlaGluValAlaValTyrtYrCyseGlnGlnTyrtYrserThr 100
QY 283 CGGTACACTTTGGCCAGGGGACCAAGCTGGAGATCAAA 321
Db 101 ProTyserPheGlyGlnGlyThrIySleuGlnIleIyS 113

RESULT 7
KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human Igm
RT anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: The second and third hypervariable regions of this
CC chain are identical with those of the human POM V-III kappa chain,
CC with which it shares certain idiotypic determinants.
CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC globulin activity.
CC PIR: A01871; KIHULY.
DR HSSP; P01607; 1BWM.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

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Alignment Scores: 8.07e-38 Length: 108
 Pred. No.: 433.00 Matches: 82
 Score:

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Percent Similarity: 86.92% Conservative: 11
Best Local Similarity: 76.64% Mismatches: 14
Query Match: 75.83% Indels: 0
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x KVIM_HUMAN (1-108)
QY 1 GAGTCCAGATGACCCAGTCTCCATCCCTGCTGCTTCTGCGGAGACAGATCAC 60
Db 1 AspllevalmetrthginserserprospserleuAlaValserleuGIuValgAlaThr 20
QY 61 ATCACTTGTCAGACAGTACGAGCAT-----AGCAGCTATTAAAT 120
Db 21 IleancyslyserSerSerInserValleuTyrserserAsnSerIysAsnTyrlenula 40
QY 121 GAGACAGCTCTCAAGCTGCTCATTTACTGGCGATCAACCGGAGATCCGGGCTCCAGC 180
Db 41 GlyleuAlaProIySleuLeuIleTyrtYrCyseGlnGlnTyrtYrserThr 60
QY 181 CGATTTCAGTGGCAGCGGGTCTGGACAGATTTCAGTCTCAGCAGAGTTCAGACATC 240
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerleuGlnPro 80
QY 241 GAAGATTCCTGCACTTACTACTGTCTCAGCAGAGTTCAGACATCCCGTACACTTTGGCCAG 300
Db 81 GlusplleAlaThrTyrtYrCyseGlnGlnTyrtYrsAsnThrProIyProIyPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 101 GlyThrIySleuValGluValIyS 107

RESULT 8
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TRENBLUREL. 27, Created)
DT 05-JUL-2004 (TRENBLUREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLUREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalela U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.

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DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-sect; 1.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IgC1; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
KW SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Alignment Scores:
Pred. No.: 8,79e-38 Length: 236
Score: 433.00 Matches: 84
Percent Similarity: 86.79% Conservative: 8
Best Local Similarity: 79.25% Mismatches: 14
Query Match: 75.83% Indels: 0
DB: Gaps: 0

US-09-403-107-141 (1-321) x O6GMX1 (1-236)
QY 4 CTCGAGTACGACGAGTCTCATCTCCGTCTGCTTGTGGAGACAGATCACCATC 63
DB 24 ILEGLIMETHTHRLINSETPROSERSEVALSERVALGLYSPHAGVALTHRLIE 43
QY 64 ACTTGTCGCAAGTACGACGATTAAGCTATTAATAATTGTATCAGCAAGAACGGA 123
DB 44 THRCYARGLASERGLNGLYLSEERASAPLEUCLYTRPYRGLNGLYNLYSPROGLY 63
QY 124 GACCTTCCTAGCTGCTCATTTTCTGCGCATCTACCCGGGAATCCGGGGTCCCTGACCA 183
DB 64 LYALAPROLYSEULEUETLYRVALAASESERLEUINSERGVALPROSEARLY 83
QY 184 TTGAGTGGGACGGGTCGGGACAGATTTCATCTCCATCAGCAGTACAGCTGAA 243
DB 84 PHSESEGLYSEGLYSEGLYTHASPHETHRIEUTRIIESESESELEUGLNPGLN 103
QY 244 GATTTCGCACTTACTACTGTGACAGAGTTACGACATCCCGTACACTTTTGGCCAGGG 303
DB 104 ASPHNEIATHRYTRYCYSLAUGLNASPTYASNTYPRTRPHRPHGLYGLNGLY 123
QY 304 ACCAAGCTGAGATCAAA 321
DB 124 THRLYVALGLIULEYS 129

RESULT 9
O6GMX8 PRELIMINARY; PRT; 236 AA.
ID O6GMX8
AC O6GMX8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshilyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.J., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RC "Generation and initial analysis of more than 15,000 full-length human
RC and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-sect; 1.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; IgC1; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
KW SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Alignment Scores:
Pred. No.: 8,79e-38 Length: 236
Score: 433.00 Matches: 82
Percent Similarity: 87.85% Conservative: 12
Best Local Similarity: 76.64% Mismatches: 13
Query Match: 75.83% Indels: 0
DB: Gaps: 0

US-09-403-107-141 (1-321) x O6GMX8 (1-236)
QY 1 GAGCTCAGATGACGACGCTCCATCTCCGTCTGCTTGTGGAGACAGATCACC 60
DB 23 ASPIILEGLIMETHTHRLINSETPROSERSEVALSERVALGLYSPHAGVALTHRLIE 42
QY 61 ATCACTTGTGCAAGTACGACGATTAAGCTATTAATAATTGTATCAGCAAGAACCA 120
DB 43 ILETHRCYARGLASERGLNGLYLSEERASAPLEUCLYTRPYRGLNGLYNLYSPRO 62
QY 121 GAGACGCTTCCTAGCTGCTCATTTTCTGCGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 63 GLYLYALAPROLYSEULEUETLYRVALAASESERLEUINSERGVALPROSEARLY 82
QY 181 CGATTTCAGTGGACGGGTCGGGACAGATTTCATCTCCATCAGCAGTACAGCTGAA 240
DB 83 ARGPHSESEGLYSEGLYSEGLYTHASPHETHRIEUTRIIESESESELEUGLNPGLN 102
QY 241 GAGATTCGCACTTACTACTGTGACAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
DB 103 GLUASPHNEIATHRYTRYCYSLAUGLNASPTYASNTYPRTRPHRPHGLYGLNGLY 122
QY 301 GGAACCAAGCTGAGATCAAA 321
DB 123 GLYTHLYVALASPILEYS 129

RESULT 10
O6GMX0 PRELIMINARY; PRT; 236 AA.
ID O6GMX0
AC O6GMX0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
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05-JUL-2004 (TRENBLER. 27, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Caranci P., Prange C.,
RA Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC073775; AAH73775.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-sect; 1.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;

Alignment Scores:
Pred. No.: 1.44e-37 Length: 236
Score: 431.00 Matches: 82
Percent Similarity: 87.85% Conservative: 12
Best Local Similarity: 76.64% Mismatches: 13
Query Match: 75.48% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x Q6GMX0 (1-236)

QY 1 GAGCTCCAGATGACCACTTCATCTCCCTGCTGCTTGTGGAGACAGATCAC 60
DB 23 AspliegimethrghinserrroserSerleuserralaserValgIyAspArgValthr 42
QY 61 ATCACTTGTGGACAGTCAAGTCAAGCATTAATAATTGATATCAGAGAAACCA 120
DB 43 IlerhrCyAsrgalaserghinserrroserSerleuserralaserValgIyAspArgValthr 62
QY 121 GAGACGCTCTTAAGTCTCTATTTATTCAGGCGATCCCGGAAATCCGGGAGTCCCTGAC 180
DB 63 GlylsalalProasmlenleuilerlyrAlaalsaserSerleugInserglYvalProser 82

QY 181 CGATTGAGTGGACGGGTCGGACAGATTTCACCTCCATCAGACAGTCAACCT 240
DB 83 ArgPheSerGlySerGlySerGlyThrAspPheThrleuThrIleSerSerleuArgPro 102
QY 241 GAAATTCCTGACACTTACTGCTGACAGAGTTCAGACATCCCGTACACTTTGGCCAG 300
DB 103 AspaPhePheAlaThrlyrYrYrCyGInGInserlyrAnlleProleuThrPheGlyly 122
QY 301 GGAACCAAGTGGAGATCAAA 321
DB 123 GlyThrAnValGluIlely 129

RESULT 11
K1LE_HUMAN STANDARD; PRT; 108 AA.
ID K1LE_HUMAN
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.,
RT "The amino acid sequence of a human kappa light chain."
RL Biochem. J. 123:945-958 (1971).
CC -1- MISCERLANEOUS: The C region of this chain has the INV (3) marker.
DR PIR; A01865; KIHUBD.
DR HSSP; P01607; IBMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFD 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E35001F1B51 CRC64;

Alignment Scores:
Pred. No.: 7.55e-37 Length: 108
Score: 424.00 Matches: 79
Percent Similarity: 85.85% Conservative: 12
Best Local Similarity: 74.53% Mismatches: 15
Query Match: 74.26% Indels: 0
Gaps: 0

US-09-403-107-141 (1-321) x K1LE_HUMAN (1-108)

QY 1 GAGCTCCAGATGACCACTTCATCTCCCTGCTGCTTGTGGAGACAGATCAC 60
DB 1 ***1le***methrghinserrroserSerleuserralaserValgIyAspArgValthr 20
QY 61 ATCACTTGTGGACAGTCAAGTCAAGCATTAATAATTGATATCAGAGAAACCA 120
DB 21 IlerhrCyAsrgalaserghinserrroserSerleuserralaserValgIyAspArgValthr 40
QY 121 GAGACGCTCTTAAGTCTCTATTTATTCAGGCGATCCCGGAAATCCGGGAGTCCCTGAC 180
DB 63 GlylsalalProasmlenleuilerlyrAlaalsaserSerleugInserglYvalProser 82

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Db      41 GLYValAlaProLysValLeuIlePheAlaAlaSerSerLeuLysSerGlyValProSer 60
QY      181 CGATTGCTGGCAGCGGGGTCTGGGACGATTTTCACTTCACCATCAGACGATCTACACCT 240
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerGlyLeuPro 80
QY      241 GAAGATTCTCGACACTTCTACTGTCAGACAGATTACAGACATCCCGTACACTTTGGCCAG 300
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrThrProTyrThrPheGlyPro 100
QY      301 GGGACCAAGCTGGAGATC 318
Db      101 GlyThrLysValGluMet 106

RESULT 12
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IBMW.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Alignment Scores:
Pred. No.: 7.55e-37 Length: 108
Score: 424.00 Matches: 84
Percent Similarity: 84.11% Conservative: 6
Best Local Similarity: 78.50% Mismatches: 17
Query Match: 74.26% Indels: 0
DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x Q9UL70 (1-108)
QY      1 GAGGTCCAGATGACCCAGTCCATCTCCCTGTGCTTCTGTGGGAGACAGAGTACC 60
Db      1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY      61 ATCACTGTGCGACACTGTCAGACAGATTAGACGATTAATTAATGGTATCAGACAAACA 120
Db      21 IleThrYsarGlnAspGlnGlnGlyIleSerAsnTyrLeuAlaIlePryrGlnGlnLysPro 40
QY      121 GACAGCCTCTTAAGCTGCTCATTTACTGGCGATCTACCCGGGAGATCCGGGGTCCCTGAC 180
Db      41 GlyLysValProLysSerLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 60
QY      181 CGATTGCTGGCAGCGGGGTCTGGGACGATTTTCACTTCACCATCAGACGATCTACACCT 240
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 80
QY      241 GAAGATTCTCGACACTTCTACTGTCAGACAGATTACAGACATCCCGTACACTTTGGCCAG 300

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Db      81 GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
QY      301 GGGACCAAGCTGGAGATCAA 321
Db      101 GlyThrLysLeuGlnIleLys 107

RESULT 13
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rel.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Bpp O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BMW; X-ray; A/B=1-107.
DR PDB; 1RE1; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006953; F:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF0047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT TURN 24 30
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57

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RL Biophys. Struct. Mech. 1:139-146(1975).

181 CGATTCACTGGCAGCGGCTCTGGACAGATTTC

Db
61 ArgPheSerGlyGlySerGlyAlaHisPheThrPheThrIleSerSerLeuGln

QY 241 GAAGATTCTGCAACTTACTGTGAGAGAGTTACGACATCCCGACACTTTTGGCCAG 300
DB 81 GUAAspIleIleAlaThrTrpTyrCysGlnGlnTyrAspTyrLeuProThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 101 GlyThrLysValGluIleLys 107
RESULT 15
KV1N_HUMAN STANDARD; PRT; 108 AA.
ID KV1N_HUMAN
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region OV.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
DR HSP: P01607; KIHUO.
DR PIR: A01872; KIHUO.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS00835; Ig_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105827E CRC64;
Alignment Scores:
Pred. No.: 2.04e-36 Length: 108
Score: 420.00 Matches: 73
Percent Similarity: 85.98% Conservative: 19
Best Local Similarity: 68.22% Mismatches: 15
Query Match: 73.56% Indels: 0
DB: 1 Gaps: 0
US-09-403-107-141 (1-321) x KV1N_HUMAN (1-108)
QY 1 GAAGCTCAGATGAGCCAGTTCATCTGCTTCTGAGGAGACAGAGTCACC 60
DB 1 AspIleGlnMetThr**SerProSerLeuSerAlaSerValGly**ArgValThr 20
QY 61 ATCACTTGTGCAAGTTCAGACATTAGCAGCTATTAAATTGTATCAGCAAAACA 120
DB 21 IleThrCysArgAlaSer**ThrIleSerSerTyrLeu**TrpTyr*****LysPro 40
QY 121 GACAGAGCTCTAGCTGCTCATTTACTGGGATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 41 GlyLysAlaPro**LeuLeuIleTyrAlaAlaSer**LeuHisSerGlyValProSer 60

QY 181 CGATTCAAGTGGAGGGGTCTGGAGACAGATTTCACTTCACCATCAGAGTCAACCT 240
DB 61 ArgPheSerGlySerGlySerLeu**PheTrpPheThrIleSerSerLeu**Pro 80
QY 241 GAAGATTCTGCAACTTACTGTGAGAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
DB 81 *****PheAlaThrTyrTyrCys*****SerTyrSerSerProThrThrPheGly*** 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
DB 101 GlyThrArgLeu**IleLys 107

Search completed: August 29, 2005, 11:06:45
Job time : 71.3611 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 95.5214 Seconds
(without alignments)
3085.293 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381

Perfect score: 696
Sequence: 1 gaggtgcagctgcgcagtc.....ccacggtcacccctctctca 381

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np model -DEV=xlp
-O=/sgn2.1/USPRO_epool_p/US09403107/runat_29082005_120124_18882/bpp_query.fasta_1.1038
-DB=A Geneseg -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=humand4.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptco -NORM=ext -HEPESIZE=500 -MINLEN=200000000
-USER=US09403107 @CGN_1_1_308 @runat_29082005_120124_18882 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseg_16Dec04:*

1: Genesegp1980s:*\n2: Genesegp1990s:*\n3: Genesegp2000s:*\n4: Genesegp2001s:*\n5: Genesegp2002s:*\n6: Genesegp2003as:*\n7: Genesegp2003bs:*\n8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	98.6	127	2	AAV17954 Human D4.
2	686	98.6	138	2	AAW80815 Amino aci
3	686	98.6	523	3	AAV44994 HD70scFv-
4	686	98.6	524	3	AAV44995 HD70scFv-
5	608.5	87.4	124	6	ADA89238 Human ant
6	598.5	86.0	122	8	ADK38663 Mouse hea
7	597.5	85.8	122	8	ADP22128 Human ant
8	597.5	85.8	122	8	ADP38664 Mouse hea
9	595.5	85.6	126	8	ADP22222 Human ant
10	594.5	85.4	143	3	AAV82629 Human PTH

11	591	84.9	451	3	AAV93734 The heavy
12	591	84.9	451	6	AAE35689 Human 11.
13	590	84.8	123	8	ADK84396 Human ant
14	590	84.8	123	8	ADK84396 Human ant
15	589.5	84.7	118	5	AAV51167 Human DP-
16	589.5	84.7	126	7	ADK18786 Ant-i-huma
17	589.5	84.7	126	7	ADK18822 Ant-i-huma
18	589.5	84.7	126	7	ADK18882 Ant-i-huma
19	589.5	84.7	126	7	ADK18953 Ant-i-huma
20	589.5	84.7	126	7	ADK18785 Ant-i-huma
21	589.5	84.7	126	7	ADK18601 Ant-i-huma
22	589.5	84.7	126	7	ADK18858 Ant-i-huma
23	589.5	84.7	126	8	ADL25404 Human mab
24	589.5	84.7	126	8	ADL25420 Human mab
25	589.5	84.7	134	8	ADP22348 Human ant
26	589	84.6	146	5	AAV51169 Human rec
27	588.5	84.6	143	3	AAV82621 Human PTH
28	588	84.5	146	5	AAV51172 Human rec
29	587.5	84.4	143	3	AAV82625 Human PTH
30	587	84.3	123	8	ADK84372 Human ant
31	587	84.3	123	8	ADK84372 Human ant
32	586.5	84.3	143	3	AAV82622 Human PTH
33	586.5	84.3	143	3	AAV82623 Human PTH
34	586	84.2	123	8	ADP22218 Human ant
35	586	84.2	146	5	AAV51171 Human rec
36	586	84.2	146	5	AAV51168 Human rec
37	586	84.2	252	5	ADP45720 Human Bly
38	586	84.2	252	7	ADG96547 Single ch
39	585.5	84.1	249	5	ADP44501 Human Bly
40	585.5	84.1	249	7	ADG95328 Single ch
41	584.5	84.0	249	5	ADP45091 Human Bly
42	584.5	84.0	249	5	ADP45104 Human Bly
43	584.5	84.0	249	5	ADP44386 Human Bly
44	584.5	84.0	249	5	ADG95213 Single ch
45	584.5	84.0	249	7	ADG95918 Single ch

ALIGNMENTS

RESULT 1	AAV17954 standard; protein; 127 AA.
ID	AAV17954
AC	AAV17954;
DT	04-AUG-1999 (first entry)
DE	Human D4.5 heavy chain variable region.
KM	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW	autoimmune disease; scfv-antibody; single-chain fv.
OS	Homo sapiens.
PN	W09925818-A1.
PD	27-MAY-1999.
PF	16-NOV-1998; 98MO-EP007313.
PR	17-NOV-1997; 97EP-00120096.
PA	(KUFE/) KUFE P.
PI	Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
DR	WPI: 1999-338004/28.
DT	N-PSDB; AAX77236.
PT	Phage display system for identification of binding site domains retaining
PS	capacity to bind an epitope.
PS	Disclosure; Fig 3.1; 152pp; English.

XX The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method

XX
SQ Sequence 127 AA;

Alignment Scores:

Pred. No.:	1.08e-62	Length:	127
Score:	686.00	Matches:	126
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.21%	Mismatches:	0
Query Match:	98.56%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-143_COPY_1_381 (1-381) x AAM17954 (1-127)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGGAGCGCTGCTCCAGGAGCTCCAGACTC 60
DB 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACAGCTCTGAGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCGAGGCT 120
DB 21 SerCysAlaIalaSerGlyPheThrPheSerSerTyrlYmethIstPValArgGlnAla 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGAGTAATAATCTAT 180
DB 41 ProGlyLysGlyLeuGlnTyrPValAlaValIleSerTyAspGlySerAsnLysTyTYr 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCACATCTCCAGAGCAAAATCCAGACGCTGTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTYr 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgIalaGlnAspThrAlaValIleTYrCysAlaIalysAspMet 100
QY 301 GGGTGGGGCAGTGGCTGGAAGACCTTACTACTACGTATGACGTCCTGGGGCCAAAGG 360
DB 101 GlyTyrGlySerGlyTyrPargProIlyrTYrTYrGlyMetAspValTyrGlyGlnGly 120
QY 361 ACCACGGTCAACGCTCTCTCA 381
DB 121 ThrThrValThrValSerSer 127

RESULT 2

AAM80815 ID AAM80815 standard; protein; 138 AA.

AC AAM80815;

DT 16-FEB-1999 (first entry)

DE Amino acid sequence of human D4.5 heavy chain variable region.

XX Human; D4.5 heavy chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease.

OS Homo sapiens.

XX WO9846645-A2.

XX 22-OCT-1998.

XX 14-APR-1998; 98MO-EP002180.

XX 14-APR-1997; 97EP-00106109.

XX (KUPE/) KUPEP P.

XX (RAUM/) RAUM T.

XX Kufer P, Raum T;

XX WPI; 1998-594564/50.

XX N-PSDB; AAV68537.

PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.

PS Claim 9; Fig 7; 84pp; English.

CC This is the amino acid sequence of the human D4.5 heavy chain variable
CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process

SQ Sequence 138 AA;

Alignment Scores:

Pred. No.:	1.1e-62	Length:	138
Score:	686.00	Matches:	126
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.21%	Mismatches:	0
Query Match:	98.56%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-143_COPY_1_381 (1-381) x AAM80815 (1-138)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGGAGCGCTGCTCCAGGAGCTCCAGACTC 60
DB 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACAGCTCTGAGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCGAGGCT 120
DB 21 SerCysAlaIalaSerGlyPheThrPheSerSerTyrlYmethIstPValArgGlnAla 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGAGTAATAATCTAT 180
DB 41 ProGlyLysGlyLeuGlnTyrPValAlaValIleSerTyAspGlySerAsnLysTyTYr 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCACATCTCCAGAGCAAAATCCAGACGCTGTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTYr 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgIalaGlnAspThrAlaValIleTYrCysAlaIalysAspMet 100
QY 301 GGGTGGGGCAGTGGCTGGAAGACCTTACTACTACGTATGACGTCCTGGGGCCAAAGG 360
DB 101 GlyTyrGlySerGlyTyrPargProIlyrTYrTYrGlyMetAspValTyrGlyGlnGly 120
QY 361 ACCACGGTCAACGCTCTCTCA 381
DB 121 ThrThrValThrValSerSer 127

RESULT 3
 AAY44994
 ID AAY44994 standard; protein; 523 AA.
 AC AAY44994;
 DT 23-MAY-2000 (first entry)
 XX
 XX HD70scFv-CH1-GM-CSF chain.
 DE
 KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpcAM;
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
 KW granulocyte/macrophage colony stimulating factor; heteromultibody;
 KW CH1-domain; multifunctional compound; heavy chain constant domain;
 KW immunoglobulin; cytosolic; immunostimulatory; antileukaemia; diagnosis;
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
 XX
 OS Homo sapiens.
 XX
 XX WO200006605-A2.
 XX
 XX 10-FEB-2000.
 XX
 XX 28-JUL-1999; 99WO-EP005416.
 XX
 XX 28-JUL-1998; 98EP-00114082.
 XX
 XX (MICR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.
 XX
 XX Kufer P, Dreier T, Baerle PA, Borschert K, Zetl F;
 DR MPI, 2000-195265/17.
 DR N-PSDB; AA250587.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 XX
 BS Example 10; Fig 55A; 166pp; English.
 XX
 CC The patent discloses heteromultibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CL-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromultibodies have
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is the left chain of a
 CC heteromultibody comprising HD70 single-chain Fv (scFv) fragment N-
 CC terminally linked to human CH1 domain which bears at its C-terminus the
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
 CC HD70 scFv specifically recognises the human epithelial cell adhesion
 CC molecule (EpcAM) also called 17-1A antigen
 XX
 XX Sequence 523 AA;
 Alignment Scores:
 Pred. No.: 1,44e-62 Length: 523
 Score: 686.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.21% Mismatches: 0
 Query Match: 98.56% Indels: 0
 DB: 3 Gaps: 0
 US-09-403-107-143_COPY_1_381 (1-381) x AAY44994 (1-523)

QY 1 GAGGTGCACTGCTCGAATCTGGGGAGAGCCCTGGTCCAGCCTGGAGAGTCCCTGAGATC 60
 Db 142 GIUValGInLeuLeuGInSerGlyGlyValValGInProGlyArgSerLeuArgLeu 161
 QY 61 TCCTGTGCAAGCCTCGATTACCTTCAGTATGAGCATGACCTGGGTCCGACAGCT 120
 Db 162 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 181
 QY 121 CCAGGCAAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATATAACTAT 180
 Db 182 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrglySerAsnLysTyrr 201
 QY 181 GCAAGTCCGTGAAGGGCCGATTCACCATCTCCGAGACAAATCCAGACACCTGTAT 240
 Db 202 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 221
 QY 241 CTGCAATATGAACACGCTGAGAGTGAAGACAGGCTGTGATTAATCTGCGAAAGATATG 300
 Db 222 LeuGlnMetCysSerLeuArgAlaGlnAspPheValValTyrTyrCysAlaLysAspPhe 241
 QY 301 GGGTGGGACAGTGGCTGGAGACCCCTACTACTACTACGATATGACGTCTGGGGCAAGG 360
 Db 242 GlyTrpGlySerGlyTrpArgProTyrTyrTyrGlyMetAspValTrpGlyGlnGly 261
 QY 361 ACCACGGTCAACCTCTCTCA 381
 Db 262 ThrThrValThrValSerSer 268
 RESULT 4
 AAY44995
 ID AAY44995 standard; protein; 524 AA.
 AC AAY44995;
 DT 23-MAY-2000 (first entry)
 XX
 XX HD70scFv-CK-interleukin 2.
 DE
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;
 KW EpcAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
 KW interleukin-2; CK-domain; kappa light chain constant domain;
 KW heteromultibody; multifunctional compound; immunoglobulin; cytosolic;
 KW immunostimulatory; antileukaemia; diagnosis; prevention;
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
 XX
 OS Homo sapiens.
 XX
 XX WO200006605-A2.
 XX
 XX 10-FEB-2000.
 XX
 XX 28-JUL-1999; 99WO-EP005416.
 XX
 XX 28-JUL-1998; 98EP-00114082.
 XX
 XX (MICR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.
 XX
 XX Kufer P, Dreier T, Baerle PA, Borschert K, Zetl F;
 DR MPI, 2000-195265/17.
 DR N-PSDB; AA250588.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 XX
 BS Example 10; Fig 55B; 166pp; English.
 XX
 CC The patent discloses heteromultibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin

CC	involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in surplus. (I) is useful for diagnosing the botulism
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (II) exhibits specificity and affinity towards BoNT/A. (I)
CC	enables rapid detection or diagnosis of botulism. This is the amino acid
CC	sequence of a mouse heavy chain variable fragment anti-botulinum toxin
XX	scFv.
XX	
SQ	Sequence 122 AA;
Alignment Scores:	
Pred. No.:	1,45e-53 Length: 122
Score:	598.50 Matches: 115
Percent Similarity:	92.13%
Best Local Similarity:	90.55% Mismatches: 2
Query Match:	85.99% Indels: 5
DG:	Gaps: 2
US-09-403-107-143_COPY_1_381 (1-381) x ADR38663 (1-122)	
OY	1 GAGTGTACACTGTGTGGAGTCGTGGGGGAGCGCTGGTCCAGCCTGGAGAGTCCCTGAGACTC 60
DB	1 : 20
OY	61 TCCCTGTGCAGCCTCTTGATTCACCTTCAGTAGCTAATGGCATGACGCTGGTCCGCCAGGCT 120
DB	21 SerCyAlaAlaSerdlPheThrheeserleryrAlamethstlrPvalAArglnAla 40
OY	121 CCAAGCAAAGGGCTGGAGTGGGTGGCAGCTTAATCATATGATGGAAATAAATACTAT 180
DB	41 ProGllylgslglLeuglultrPvalAlaValllleSerrYrapgJlserrAnlytYrTy 60
OY	181 GCAGACTCCGTGAAGGGCCGATTCACATTCGCCAGACAATTCCAGAACAGCGCTAT 240
DB	61 AlaasServallysdlYArPhetheThrilleSerArghaspanserlYbaentHrLueTy 80
OY	241 CTGCAATGAACAGCCTGAGAGCTGAGAGCACAGCGCTGTGTATTCCTGTGGAAAGATATG 300
DB	81 LeuglImeeAshserleuhrgAlaclunaphrhAlavalTYrCYbalaaaghsp--- 99
OY	301 GGGTGGGGGAGTGGCTGGAGAACCTTACTACTACTACGGTATGACGCTTGGGGGCAAAGG 360
DB	100 ---TripserglUgly-----TYrtyrTYrtyrTYrTYrTYrTYrTYrTYrTYrTYr 115
OY	361 ACCACGGGTCAACCGTCTCTCTCA 381
DB	116 ThrThrvallllevalSerSer 122
RESULT 7	
ID ADP22128 standard; protein; 122 AA.	
ADP22128	
AC ADP22128;	
DT 09-SEP-2004 (first entry)	
XX Human anti-TNFa antibody heavy chain variable region SEQ ID NO:34.	
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;	
KW anti-TNFa antibody; anabolic; antihyperoslerotic; antiarthritis;	
KW antibacterial; antiinflammatory; antiporiatic; antineumatic;	
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;	
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;	
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;	
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;	
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;	
KW prostatic cancer; immuno-mediated inflammatory disease;	
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;	
KW reestenosis; autoimmune disease; Crohn's disease; graft-host reaction;	
KW septic shock; cachexia; anorexia; multiple sclerosis.	
XX	

OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 PA (ABGE-) ABGENIX INC.
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 DR N-PDB; ADP22127.
 XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 34; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNF α) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNF α in a patient sample, comprising contacting with
 CC (1), and detecting the level of binding between the antibody and TNF α in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF α induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF α induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antihypertensive, antidiabetic, antirheumatic,
 CC antibacterial, antiinflammatory, antiproliferative, antithrombotic,
 CC disorder, immunomodulatory, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNF α antagonist. The antibody (II) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNF α
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 122 AA:

Alignment Scores:
 Pred. No.: 1.84e-53 Length: 122
 Score: 597.50 Matches: 114
 Percent Similarity: 92.91% Conservative: 4
 Best Local Similarity: 89.76% Mismatches: 5
 Query Match: 85.85% Indels: 4
 DB: Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x ADP22128 (1-122)

QY 1 GAGGTGAGCTGCTCGAGCTCGGGGAGGCGCTGCTCCAGCTGGAGGCTCCCTGAGACTC 60
 DB 1 GlnValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

QY 61 TCCTGTGACAGCTCTGATTCACCTTACAGTACGTATGCATGCGACGTCCGACGCT 120
 DB 21 SerCysAlaAlaSerClyPheThrPheSerSerTyrGlyMetHisTyrValArgGlnAla 40
 QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCGACTTATATCATATGATGAAAGTAAATATCTAT 180
 DB 41 ProGlyLysGlyLeuGlnLutryPValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
 QY 181 GCAGACTCCGTAAAGGGCCGATTCACCATCTCCAGAGCAATTCACGAAGACGCGTAT 240
 DB 61 AlaAspSerValIleSerLysPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
 QY 241 CTGCAATGATGACAGCTGAGACCTGAGACGACGAGTGTGTATTAATCTGCGAAGATATG 300
 DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspGln 100
 QY 301 GGGTGGGCGACGTGGCTGAGACCTTACTACTACTACGCTATGAGAGCTGGGGCCAGGG 360
 DB 101 -----AspAsnTrpAsn-----TyrTyrTyrGlyMetAspValTrpGlyGlnGly 115
 QY 361 ACCAGGTCACCGTCTCCCTCA 381
 DB 116 ThrThrValThrValSerSer 122

RESULT 8
 ADR38664
 ID ADR38664 standard; peptide; 122 AA.

AC ADR38664;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region scFv seqid 66.

KX antibacterial; antibody; botulinum neurotoxin type A; BONT/A.
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KN heavy chain variable region; single chain antibody; scFv.

XX Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNITV CALIFORNIA.

PI Marks JD, Amersdorfer P;

DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 66; 110pp; English.

PS The invention describes an isolated antibody (I) that specifically binds
 XX to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (II) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-

CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
CC scFv.

SQ Sequence 122 AA;

Alignment Scores:
Pred. No.: 1,84e-53 Length: 122
Score: 597.50 Matches: 113
Percent Similarity: 92.91% Conservative: 5
Best Local Similarity: 88.98% Mismatches: 4
Query Match: 85.85% Indels: 5
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x ADR38664 (1-122)

QY 1 GAGTCGACGCTGCTGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60
DB 1 GlnIleGlnLeuLeuGlnSerSerIlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATGATCACTTCAGTAGCTATGCGACTGCGCGAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyraIaMeH1aItrValaArg1nAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGCGACTTATCATATGATGAGAAATTAATACAT 180
DB 41 ProGlyIysGlyLeuGlnItrPalaIaValIleSerTyraPbGlySerAsnIySerTyrr 60
QY 181 GCAGACTCCGTGAAGGGCGATTCAATCTCCAGAGCAATTCAGAGACGCTGAT 240
DB 61 AlaAspSerValIyGlyArgPheThrIleSerArgAspAsnSerIyAsnThrIleuTyrr 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCCAAGATATG 300
DB 81 LeuGlnMetAanSerLeuArgIaGlyAspThrIraIaValTyrrTyCyaAlaArgAsp--- 99
QY 301 GGGTGGGGCAGTGGCTGAGACCCACTACTACGCTATGAGACTGCTGGGCCAAGGG 360
DB 100 ---TTPserGluGly-----TyrrTyrrTyrrGlyMetAspValItrpIyGlnIly 115
QY 361 ACCACGTCACCGTCTCTCA 381
DB 116 ThrThrValIleValSerSer 122

RESULT 9
ADP22222
ID ADP22222 standard; protein; 126 AA.
XX
XX ADP22222;
XX AC
XX ADP22222;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:128.
XX
XX human; monoclonal antibody; tumour necrosis factor- α ; TNFA;
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritis;
XX antibacterial; antiinflammatory; antiporiatic; antineumatic;
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
XX neuroprotective; vasotropic; antileptotic; TNFA antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;

KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

FN WO2004050683-A2.

PD 17-JUN-2004.

PP 02-DEC-2003; 2003WO-US038281.

PR 02-DEC-2002; 2002US-0430729P.

PA (ABGE-) AGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendsch M, Kathanaswami P, Pigott C, Liang ML, Lee R;

PI Manchulenko K, Paggioli R, Senaldi G, Qiaojuan JS;

DR WPI; 2004-480601/45.

DR N-PSDB; ADP22221.

PT New recombinant human monoclonal antibody that specifically binds to

PT Tumor Necrosis Factor- α , useful for treating neoplastic disease such

PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid

PT arthritis.

PS Example 10; SEQ ID NO 128; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor- α (TNFA) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP2417) or (S2, ADP2421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP2418) or (S4, ADP2424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFA induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritis,
CC antibacterial, antiinflammatory, antiporiatic, antineumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

SQ Sequence 126 AA;

XX Alignment Scores:

Pred. No.: 3e-53 Length: 126
Score: 595.50 Matches: 113
Percent Similarity: 93.70% Conservative: 6
Best Local Similarity: 88.98% Mismatches: 7
Query Match: 85.56% Indels: 1
Gaps: 1

US-09-403-107-143_copy_1_381 (1-381) x ADP22222 (1-126)

QY 1 GAGGTGCACTGCTCGAGTCTGGGGAGGCGCTGCTCGAGGCTGGAGGCTCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGCAAGCCCTGTGATTCACCTTCAGTACGATGAGCATGAGCATGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrGlyMetHisTrpValAlaGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCATTATATCATATGATGAAATAAATATCTAT 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaValAlaIleTrpTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCGAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAGAACAGCTGTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAAACGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgGlu--- 99
QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGATGAGCATGAGCGTGGGGCCAAAGG 360
DB 100 GlyTlAlaValAlaGlyProProTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGly 119
QY 361 ACCACGGTCAACCGTCTCTCA 381
DB 120 ThrThrValThrValSerSer 126

RESULT 10
AAV82629 standard; protein; 143 AA.

AC AAV82629;
DT 02-AUG-2000 (first entry)
XX

DE Human PTHrP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:42.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
XX fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;
XX systemic inflammatory response syndrome; SIRS; hypophosphataemia;
XX antiarthritic; cytostatic; antiinflammatory.
XX
XX Homo sapiens.
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-00304793.
XX
XX 17-JUN-1998; 98JP-00188196.
XX
XX 26-JUN-1998; 98JP-00196729.
XX
XX (NIBS) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX
XX N-PSDB; AAA13939.
XX
XX A human monoclonal antibody to parathyroid hormone related protein. -
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain.
XX
XX Claim 32; Page 76-77; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a human
CC PTHrP monoclonal antibody clone protein sequence from the present
CC invention
XX
XX Sequence 143 AA;
SQ
Alignment Scores:
Pred. No.: 3,91e-53 Length: 143
Score: 594.50 Matches: 113
Percent Similarity: 92.13% Conservative: 4
Best Local Similarity: 88.98 Mismatches: 7
Query Match: 85.42% Indels: 3
DB: Gaps: 1

US-09-403-107-143_copy_1_381 (1-381) x AAV82629 (1-143)

QY 1 GAGGTGCACTGCTCGAGTCTGGGGAGGCGCTGCTCGAGGCTGGAGGCTCCTGAGACTC 60
DB 20 GlnValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeu 39
QY 61 TCCTGTGCAAGCCCTGTGATTCACCTTCAGTACGATGAGCATGAGCATGGGTCGCCAGGCT 120
DB 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrGlyMetHisTrpValAlaGlnAla 59
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCATTATATCATATGATGAGAAATAAATATCTAT 180
DB 60 ProGlyLysGlyLeuGluTrpValAlaValAlaIleTrpTyrAspGlySerAsnLysTyrTyr 79
QY 181 GCGAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAGAACAGCTGTAT 240
DB 80 ValAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 99
QY 241 CTGCAATGAAACGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAGATATG 300
DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgGlu--- 118
QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGATGAGCATGAGCGTGGGGCCAAAGG 360
DB 119 -----SerSerGlyTyrGlnAspTyrTyrTyrGlyMetAspValTrpGlyGlnGly 136
QY 361 ACCACGGTCAACCGTCTCTCA 381
DB 137 ThrThrValThrValSerSer 143

RESULT 11
AAV93734 standard; protein; 451 AA.

ID AAV93734
AC AAV93734;
DT 03-OCT-2000 (first entry)
XX
XX The heavy chain of immunoglobulin clone 11.2.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX
XX Homo sapiens.
XX
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US030895.
XX
XX 23-DEC-1998; 98US-0113647P.
XX

PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,
PI Corvalan JR;
XX
XX WPI, 2000-442647/38.
DR N-PSDB; AAA46898.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX
XX Claim 2; Fig 22q; 157pp; English.
XX
XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
XX SQ Sequence 451 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1,156-52 Length: 451
XX Score: 591.00 Matches: 113
XX Percent Similarity: 93.70% Conservative: 6
XX Best Local Similarity: 88.98% Mismatches: 2
XX Query Match: 84.91% Indels: 2
XX DB: 3 Gaps: 1
XX
XX US-09-403-107-143_COPY_1_381 (1-381) x AA93734 (1-451)
OY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
OY 61 TCCTGTGACGCTCTGAGATTCACCTTCAGTACTGAGCATGCGATCGGCTCCGACGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40
OY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAATTAATAACTAT 180
DB 41 ProGlylybGlyLeuGlnTrpValAlaValIleTrpTyraGlySerAsnIleTyrr 60
OY 181 GCAGACTCCGTGAAGGGCGGATTCACATCTCCAGAGACAAATTCAGAGACGCTGTAT 240
DB 61 AlaAspSerVallyGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTy 80
OY 241 CTGCAAAAGAACGCTGAGAGCTGAGACACGCGTGTGTATTACTGTGCCAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrrCysAlaArgAspPro 100
OY 301 GGGTGGGCGACGTGAGTGGAGACCTTACTACTACGATGAGATGAGAGCTGGGGCGAAGG 360
DB 101 ArgGlyAlaThrLeuTyrr-----TyrrTyrrTyrrGlyMetAspValTrpGlyGlnIly 118
OY 361 ACCAGCTCACCGTCTCTCTCA 381
DB 119 ThrThrValThrValSerSer 125
XX
XX RESULT 12
XX AAE35889
XX ID AAE35889 standard; protein; 451 AA.
XX AC AAE35889;
XX

DT 17-UN-2003 (first entry)
XX
XX Human 11.2.1 anti-CTLA-4 antibody mature heavy chain.
DE
XX
XX Human, cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KM cancer.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 26..35
FT /note="Complementarity determining region (CDR) 1"
FT Region 50..64
FT /note="Complementarity determining region (CDR) 2"
FT Region 100..104
FT /note="Complementarity determining region (CDR) 3"
XX
XX EP1262193-A1.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253652.
XX
XX 23-MAY-2001; 2001US-0293042P.
XX
XX (PFIZ) PFIZER PROD INC.
XX
XX Hanson DC, Mueller EE;
XX
XX WPI, 2003-131215/13.
XX
XX N-PSDB; AAD54349.
XX
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
PT preparation of medicament for the treatment of cancer.
XX
XX Disclosure; Fig 1Q; 76pp; English.
XX
XX The invention relates to the use of human anti-cytotoxic T lymphocyte
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC cancer, cancer of the anal region, stomach cancer, breast cancer,
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC The present sequence is human anti-CTLA-4 antibody mature heavy chain
XX
XX SQ Sequence 451 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1,156-52 Length: 451
XX Score: 591.00 Matches: 113
XX Percent Similarity: 93.70% Conservative: 6
XX Best Local Similarity: 88.98% Mismatches: 2
XX Query Match: 84.91% Indels: 2
XX DB: 6 Gaps: 1
XX
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OY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
OY 61 TCCTGTGACGCTCTGAGATTCACCTTCAGTACTGAGCATGCGATCGGCTCCGACGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40
OY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAATTAATAACTAT 180
DB 41 ProGlylybGlyLeuGlnTrpValAlaValIleTrpTyraGlySerAsnIleTyrr 60
OY 181 GCAGACTCCGTGAAGGGCGGATTCACATCTCCAGAGACAAATTCAGAGACGCTGTAT 240
DB 61 AlaAspSerVallyGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTy 80
XX

QY 241 CTGCAATGAAACGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGIuMeTAsnSerLeuAlaGluAspThrAlaValTyrCysAlaAspPro 100
QY 301 GGGTGGGCGAGTGTGAGACCTTACTACTACGCTATGACGCTGTGGGCGCAAGG 360
Db 101 ArgGIyAlaThrLeuTyr-----TyrTyrTyrTyrClyMetAspValTlPglYgIngly 118
QY 361 ACCGAGGTCAACCGTCTCTCTCA 381
Db 119 ThrThrValThrValSerSer 125
RESULT 13
ADS84396
ID ADS84396 standard; protein; 123 AA.
XX
AC ADS84396;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:35.
XX
XX human; erythropoietin receptor; EPO receptor;
KM erythropoietin receptor binding antibody; EPO receptor binding antibody;
KM antihaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
KM wound healing; neural cell damage protection;
KM neural tissue damage protection; brain injury; spinal cord injury;
KM stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
XX
OS Homo sapiens.
XX
PN WC004035603-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003MO-US032243.
XX
PR 14-OCT-2002; 2002US-00269711.
PR 10-OCT-2003; 2003US-00684109.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Deviles PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX
XX WPI: 2004-134843/32.
DR N-PSDB; ADS84395.
XX
XX New antibodies that bind to or activate an endogenous human
PT erythropoietin receptor, useful for diagnosing, preventing or treating
PT disorders associated with dysfunctional erythropoietin receptor, e.g.
PT anemia.
PS Claim 9, SEQ ID NO 35; 192pp; English.
XX
XX The present invention describes an antibody or its fragment that binds to
CC or activates an endogenous activity of a human erythropoietin (EPO)
CC receptor in a mammal, but does not interact with a peptide having a
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
CC methods of modulating or activating an endogenous activity of a human EPO
CC receptor in a mammal, comprising administering to the mammal a
CC therapeutic amount of the above antibody or its fragment to modulate or
CC activate the receptor; (2) a method of treating a mammal suffering from
CC aplasia, comprising administering to the mammal a therapeutic amount of
CC the above antibody or its fragment to modulate or activate the receptor;
CC (3) a pharmaceutical composition comprising a therapeutic amount of the
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
CC an isolated and purified polynucleotide sequence; and (5) an isolated and
CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antihaemic, neuroprotective and vulnerary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence represents a human anti-EPO-R antibody heavy
CC chain variable region, which is given in the exemplification of the
CC present invention.
XX
SQ Sequence 123 AA;
Alignment Scores:
Pred. No.: 1,12e-52 Length: 123
Score: 590.00 Matches: 114
Percent Similarity: 92.13% Conservative: 3
Best Local Similarity: 89.76% Mismatches: 6
Query Match: 84.77% Indels: 4
DB: Gaps: 1
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Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAlaGlu 20
QY 61 TCCTGTGACAGCTGTGATTCACCTTCAGTAGCTATGCGATGACCTGCGCCAGGCT 120
Db 21 SerCylAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGCGATTATTCATATGATGAGAACTAATAATCTTT 180
Db 41 ProGlyLyGlyLeuGlyLeuGlyLeuTrpValAlaValAlaValIleSerTyrAspGlySerAsnTyrTyr 60
QY 181 GCAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGCAATTCGAAGAACGCGTCT 240
Db 61 AlaAspSerValIleGlyArgPheThrIleSerArgAspAsnSerIleAsnThrLeuTyr 80
QY 241 CTGCAATGAAACGCTGAGAGCTGAGAGCACGCGTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGIuMeTAsnSerLeuAlaGluAspThrAlaValTyrCysAlaAspPro 99
QY 301 GGGTGGGCGAGTGTGAGACCTTACTACTACTACGCTATGAGCGTCTGGGGCGCAAGG 360
Db 100 -----HisGlyGlyArgTyrValTyrAspTyrGlyMetAspValTlPglYgIngly 116
QY 361 ACCGAGGTCAACCGTCTCTCTCA 381
Db 117 ThrThrValThrValSerSer 123
RESULT 14
ADR68538
ID ADR68538 standard; protein; 123 AA.
XX
AC ADR68538;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-EPO-R-antibody heavy chain variable region seqid 35.
XX
XX antihaemic; respiratory; vulnerary; gene therapy; vaccine;
KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KM hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KM wound healing; neural cell damage; tissue damage; brain injury;
KM spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
KM variable region.
XX
OS Homo sapiens.
XX
PN US2004175379-A1.
XX
PD 09-SEP-2004.
XX
DT 10-OCT-2003; 2003US-00684109.
XX

XX The present sequence is that of a human DP-46 heavy chain variable region
 CC encoded by a human germline DP-46 gene in a transgenic mouse used in
 CC human monoclonal antibody (mAb) construction. A GenTIV fusion was
 CC performed using spleen cells from a hybrid mouse containing human
 CC variable and constant region antibody transgenes that was immunised with
 CC recombinant human tumor necrosis factor (TNF) alpha. Human mAbs were
 CC obtained that bound immobilised human TNF alpha with apparently high
 CC avidity. These mAbs had a totally human IgG1, kappa isotype. Their heavy
 CC chain variable region deduced amino acid sequences (see AAM51168-72)
 CC showed high similarity to the DP-46 sequence. The invention provides
 CC isolated human, primate, rodent, mammalian, chimeric, humanised and/or
 CC complementarily determining region (CDR)-grafted anti-TNF antibodies,
 CC immunoglobulins, and cleavage products and variants, as well as anti-TNF
 CC antibody compositions, encoding or complementary nucleic acids, vectors,
 CC host cells, compositions, formulations, devices, transgenic animals,
 CC transgenic plants, and methods of making and using them. The anti-TNF
 CC antibody comprises at least a portion of an immunoglobulin molecule,
 CC especially the heavy chain and/or light chain variable regions given in
 CC the present sequence and in AAM5165, or either all of the CDRs of the
 CC heavy chain (see AAM5158-60) or all of the CDRs of the light chain (see
 CC AAM5161-63). The antibodies may inhibit TNF-induced cell adhesion
 CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index
 CC improvement in a mouse model. They are useful for diagnosing or treating
 CC a TNF related condition in a cell, tissue, organ or animal (claimed) such
 CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,
 CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular
 CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina
 CC pectoris or myocardial infarction, an infectious disease in a cell such
 CC as bacterial, viral, and fungal infections, pneumonia, leprosy and
 CC malaria, a malignant disease such as leukaemia, chronic myelocytic
 CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological
 CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,
 CC Alzheimer's disease and Creutzfeldt-Jakob disease

XX Sequence 118 AA:

Alignment Scores:
 Pred. No.: 1,25e-52 Length: 118
 Score: 589.50 Matches: 113
 Percent Similarity: 91.34% Conservative: 3
 Best Local Similarity: 88.98% Mismatches: 2
 Query Match: 84.70% Indels: 9
 DB: 5 Gaps: 1

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 Db 1 GlnVal[GlnLeuVal]GlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
 QY 61 TCCTGGGACGCTCTGATTCACCTTCAGTATGAGCATGAGCTGGGCTCCGCGGCT 120
 Db 21 SerCysValAlaIleSerGlyPheThrPheSerSerTrpAlaMetHisTrpValArgGlnAla 40
 QY 121 CCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGTAATAACTAT 180
 Db 41 ProGlyIlyseGlyLeuGlnTrpValAlaValIleSerTrpaspGlySerAenlystyTytr 60
 QY 181 GCAGACTCCGTAAGGGCCGATTCACCATTCACAGACAAATTCAGAAACACGCTGAT 240
 Db 61 AlaAspSerValIlyseGlyArgPheThrIleSerArgSpasSerIlysaenThrLeuTytr 80
 QY 241 CTGCAATGTAACGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGCAAAAGATATG 300
 Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTytrCysAla----- 97
 QY 301 GGGTGGGGCAGTGGCTGACCTACTACTACTACGATGAGCGTGGGGCCAGGG 360
 Db 98 -----ArgTytrTytrTytrTytrGlyMetAspValTrpGlyGlnGly 111
 QY 361 ACCACGGTCAACGGTCTCTCA 381

Db 112 ThrThrValThrValSerSer 118
 Search completed: August 29, 2005, 11:37:18
 Job time : 98.5214 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 20.3526 Seconds

(without alignments)
2794.861 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381

Perfect score: 696
Sequence: 1 gaggtgcagctgcagctcgcagtc.....ccacgctcagctctctctca 381

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591	84.9	451	4	US-09-472-087-70
2	581.5	83.5	126	3	US-09-240-274-26
3	575.5	82.7	126	3	US-09-240-274-153
4	573.5	82.4	126	3	US-09-240-274-25
5	570	81.9	123	4	US-09-424-840B-6
6	558.5	80.2	124	4	US-09-424-840B-16
7	554	79.6	167	4	US-09-472-087-60
8	553.5	79.5	310	3	US-09-073-029-11
9	552.5	79.4	128	4	US-09-840-459-77
10	552.5	79.4	128	4	US-09-840-459-79
11	552.5	79.4	128	4	US-09-497-625A-77
12	552.5	79.4	128	4	US-09-497-625A-79

13	552	79.3	125	3	US-09-240-274-140	Sequence 140, App
14	547	78.6	120	1	US-07-942-245-35	Sequence 35, App1
15	546	78.4	123	4	US-09-560-198A-2	Sequence 2, App1
16	545	78.3	119	1	US-08-331-398A-46	Sequence 46, App1
17	545	78.3	119	2	US-08-331-397B-46	Sequence 46, App1
18	545	78.3	119	2	US-08-759-804A-46	Sequence 46, App1
19	545	78.3	119	3	US-09-227-693-46	Sequence 46, App1
20	544.5	78.2	126	3	US-09-240-274-152	Sequence 152, App
21	543	78.0	115	4	US-09-726-219A-167	Sequence 167, App
22	542	77.9	117	3	US-09-025-769B-24	Sequence 24, App1
23	542	77.9	117	4	US-09-490-070A-24	Sequence 24, App1
24	542	77.9	117	4	US-09-490-153-24	Sequence 24, App1
25	542	77.9	117	4	US-09-490-324-24	Sequence 24, App1
26	542	77.9	125	4	US-09-840-459-84	Sequence 84, App1
27	542	77.9	125	4	US-09-497-625A-84	Sequence 84, App1
28	541.5	77.8	126	3	US-09-240-274-13	Sequence 13, App1
29	541.5	77.8	126	3	US-09-240-274-16	Sequence 16, App1
30	541.5	77.8	126	3	US-09-240-274-147	Sequence 147, App
31	541.5	77.8	126	3	US-09-240-274-148	Sequence 148, App
32	540.5	77.7	126	3	US-09-240-274-146	Sequence 146, App
33	540	77.6	125	3	US-09-240-274-8	Sequence 8, App1
34	540	77.6	125	3	US-09-240-274-20	Sequence 20, App1
35	540	77.6	125	3	US-09-240-274-21	Sequence 21, App1
36	540	77.6	125	3	US-09-240-274-22	Sequence 22, App1
37	540	77.6	167	4	US-09-472-087-9	Sequence 9, App1
38	539	77.4	125	4	US-09-840-459-76	Sequence 76, App1
39	539	77.4	125	4	US-09-497-625A-76	Sequence 76, App1
40	538.5	77.4	123	3	US-08-983-607-38	Sequence 38, App1
41	537.5	77.2	174	4	US-09-472-087-12	Sequence 12, App1
42	536.5	77.1	126	3	US-09-240-274-14	Sequence 14, App1
43	536.5	77.1	126	3	US-09-240-274-15	Sequence 15, App1
44	536	77.0	225	4	US-09-456-090A-108	Sequence 108, App
45	536	77.0	225	4	US-09-453-234-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEYEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: COVATIN, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-70
Alignment Scores:
Pred. No.: 5.99e-59
Score: 591.00
Percent Similarity: 93.70%
Best Local Similarity: 88.98%
Query Match: 84.91%
DB: 4
Gaps: 1
US-09-403-107-143_COPY_1_381 (1-381) x US-09-472-087-70 (1-451)
Length: 451
Matches: 113
Conservative: 6
Mismatch: 2
Indels: 1

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Db 1 GluValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCCGCAAGCT 120
   ::::::::::::::::::::
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGTAAATATCTAT 180
   ::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleTrpTyrAspGlySerAsnLysHisTrp 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGCAATCCAGAACAGCTGTAT 240
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   ::::::::::::::::::::
Db 81 LeuGlnMetAspSerLeuArgIaGlnAspThrAlaValIleTyrCysAlaArgAspPro 100
QY 301 GGGTGGGCGAGTGGCTGAGACCCCTACTACTACTACGCTATGAGCTGGGGCGAAGG 360
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Db 101 ArgGlyAlaThrLeuTyr-----TyrTyrTyrTyrGlyMetAspValIleTrpGlyGlnGly 118
QY 361 ACCAGCGTCACCGTCTCTCTCA 381
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Db 119 ThrThrValThrValSerSer 125
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RESULT 2

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US-09-240-274-26
; Sequence 26, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26
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Alignment Scores:

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Pred. No.: 4,73e-58
Score: 581.50
Percent Similarity: 93.70%
Best Local Similarity: 86.61%
Query Match: 83.55%
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Matches: 126
Conservative: 110
Mismatches: 9
Indels: 7
Gaps: 1
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US-09-403-107-143_COPY_1_381 (1-381) x US-09-240-274-26 (1-126)

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QY 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGCAGGCTGGAGAGTCCCTGAGACTC 60
   ::::::::::::::::::::
Db 1 GluValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCCGCAAGCT 120
   ::::::::::::::::::::
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGTAAATATCTAT 180
   ::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleTrpTyrAspGlySerAsnLysHisTrp 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGCAATCCAGAACAGCTGTAT 240
   ::::::::::::::::::::
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTCGAAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
   ::::::::::::::::::::
Db 81 LeuGlnMetAspSerLeuArgIaGlnAspThrAlaValIleTyrCysAlaArgAspPro 100
```

```
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleTyrTyrAspGlySerAsnLysHisTrp 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGCAATCCAGAACAGCTGTAT 240
   ::::::::::::::::::::
Db 61 SerAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTCGAAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
   ::::::::::::::::::::
Db 81 LeuGlnMetAspSerLeuArgIaGlnAspThrAlaValIleTyrCysAlaArgGlnArg 100
QY 301 GGGTGGGCGAGTGGCTGAGACCCCTACTACTACTACGCTATGAGCTGGGGCGAAGG 360
   ::::::::::::::::::::
Db 101 AsnPheArgSerGlyTyr---SerArgTyrTyrTyrGlyMetAspValIleTrpGlyProGly 119
QY 361 ACCAGCGTCACCGTCTCTCTCA 381
   ::::::::::::::::::::
Db 120 ThrThrValThrValSerSer 126
```

RESULT 3

```
US-09-240-274-153
; Sequence 153, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153
```

Alignment Scores:

```
Pred. No.: 2.3e-57
Score: 575.50
Percent Similarity: 92.91%
Best Local Similarity: 85.83%
Query Match: 82.69%
```

```
Matches: 126
Conservative: 109
Mismatches: 8
Indels: 1
Gaps: 1
```

US-09-403-107-143_COPY_1_381 (1-381) x US-09-240-274-153 (1-126)

```
QY 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGCAGGCTGGAGAGTCCCTGAGACTC 60
   ::::::::::::::::::::
Db 1 GluValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCCGCAAGCT 120
   ::::::::::::::::::::
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGTAAATATCTAT 180
   ::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleTyrTyrAspGlySerAsnLysHisTrp 60
QY 181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGCAATCCAGAACAGCTGTAT 240
   ::::::::::::::::::::
Db 61 SerAspSerValLysGlyArgPheThrIlePheArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTCGAAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
   ::::::::::::::::::::
Db 81 LeuGlnMetAspSerLeuArgIaGlnAspThrAlaValIleTyrCysAlaArgGlnArg 100
```

Qy 301 GGGTGGGAGTGGCTGAGAGACCTACTACTAGCATGAGTGGGGCCAGAGG 360
Db 101 AasnpheargsergltYr---SeargrtYrYrYrGlymetAspValtrpGlyProGly 119
Qy 361 ACCACGGTCACCGTCTCTCA 381
Db 120 ThrThrValThrValSerSer 126

RESULT 4

US-09-240-274-25
; Sequence 25, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-25

Alignment Scores:
Pred. No.: 3,896-57 Length: 126
Score: 573.50 Matches: 109
Percent Similarity: 92.91% Conservative: 9
Best Local Similarity: 85.83% Mismatches: 8
Query Match: 82.40% Indels: 1
Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-240-274-25 (1-126)

Qy 1 GAGGTGAGCTGCTGAGATCTGGGGAGCCCTGGCCAGCTTCCCTGAGATC 60
Db 1 GlnValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCTGTGAGCCTCTGATTCACCTTCAGTAGCTATGCGATGCGGTCGCGCAGGCT 120
Db 21 SerGysAlaAlaSerGlyPheThrPheSerSerTyrglyMetArgTrpValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGCTGAGCTATATCATATGATGAGATTAATTAATCTAT 180
Db 41 ProGlyGlyGlyLeuGlnTrpValAlaValAlaValTyrglyArgGlySerAlaLysHisTyr 60
Qy 181 GCAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACAGCTGAT 240
Db 61 SerAspSerValTyrglyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAATGAACAGCCTGAGAGCTGAGACACGCGTGTGATTAATCTGCGAAGATATG 300
Db 81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrglyArgAlaArgGlnArg 100
Qy 301 GGGTGGGAGTGGCTGAGAGACCTACTACTACTAGCATGAGTGGGGCCAGAGG 360
Db 101 AasnpheargsergltYr---SeargrtYrYrYrGlymetAspValtrpGlyProGly 119
Qy 361 ACCACGGTCACCGTCTCTCA 381
Db 120 ThrThrValThrValSerSer 126

RESULT 5
US-09-424-840B-6

; Sequence 6, Application US/09242480B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-6

Alignment Scores:
Pred. No.: 9,716-57 Length: 123
Score: 570.00 Matches: 111
Percent Similarity: 91.41% Conservative: 6
Best Local Similarity: 86.72% Mismatches: 5
Query Match: 81.90% Indels: 6
Gaps: 3

US-09-403-107-143_COPY_1_381 (1-381) x US-09-424-840B-6 (1-123)

Qy 1 GAGGTGAGCTGCTGAGATCTGGGGAGCCCTGGCCAGCTTCCCTGAGATC 60
Db 1 GlnValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCTGTGAGCCTCTGATTCACCTTCAGTAGCTATGCGATGCGGTCGCGCAGGCT 120
Db 21 SerGysAlaAlaSerGlyPheThrPheSerSerTyrglyMetArgTrpValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGCTGAGCTATATCATATGATGAGATTAATTAATCTAT 180
Db 41 ProGlyGlyGlyLeuGlnTrpValAlaValAlaValTyrglyArgGlySerAlaLysHisTyr 60
Qy 181 GCAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACAGCTGAT 240
Db 61 AlaAspSerValTyrglyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAATGAACAGCCTGAGAGCTGAGACACGCGTGTGATTAATCTGCGAAGATATG 300
Db 81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrglyArgAlaArgGlnArg 100
Qy 301 GGG---TGGGGAGTGGCTGAGAGACCTACTACTACTAGCATGAGTGGGGCCAG 357
Db 101 GlySerTrpGly---GlyTrpAspHisTyr-----MetAspValTrpGlyLys 115
Qy 358 GGGACACGGTCACCGTCTCTCA 381
Db 116 GlyThrThrValThrValSerSer 123

RESULT 6
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1

```

PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 124
TYPE: PRF
ORGANISM: Homo sapiens
US-09-424-840B-16

Alignment Scores:
Pred. No.:      2,01e-55          Length:      124
Score:           558.50         Matches:       110
Percent Similarity: 90.55%     Conservative:   5
Best Local Similarity: 86.61%    Mismatch:      9
Query Match:      80.24%        Indels:        3
DB:                4            Gaps:          1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-424-840B-16 (1-124)

QY      1 GAGGTGACGTCTGTCACAGTCTGGGGGAGCGCTGGTCCAGCCTGGGAGGTCCTTGAGACTC 60
Db      1 GlnValIlyleuLeuGluSerIyglYlVaIH.sPrOgIYAgsSerIeuAryLeu 20
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      61 TCCGTGACAGCCTCTGAATTCACCTTCAGTAAGCATGACATGCATCGGTCCGCACGCT 120
Db      21 SerCyAlaIalaSerGIyPheThrPheserSerTyrrHmeHIstRpvaIArgIla 40
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      121 CCAAGGCAGGGGCTGAGATGGGTGGGACGTTATATCATATGATGAAAGTAATAACTAT 180
Db      41 PrOGIlyseGIyleuGIutrpValalaleuIIeserTYAspGIysefAmnIysrTYr 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      181 GGAGACTCGGTGAAGGGCGGATTCAACATCTCCAGAGCAATCCAGAACAAGCTGAT 240
Db      61 AlaAspserValIlysgIyArpNealalIeserAagAspAsnSerLySAsnthreunyr 80
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      241 CTGCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
Db      81 lengImechamserIeuArghIaIuaSpThraIvalTYrCYeAlaIyAspGIy 100
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      301 GGGTGGGGCAGTGGCTGGAGAACCTTACTACTACGGATATGAGAGTCTGGGGCCAAGGG 360
Db      101 ArgSerGIySerTyrrAlaArg-----PheaSpGIymeAspValTrpGIyGIngIy 117
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      361 ACCACGGTCACGCTCTCTCA 381
Db      118 ThrThrValThrValSerSer 124
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 7
US-09-472-087-80
Sequence 80, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MOELLER, EILEEN E.
APPLICANT: HANKS, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOPREY
APPLICANT: CORVALAN, JOSE R.
TITLE OR INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 167

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: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-472-087-80

Alignment Scores:
Pred. No.: 7,29e-55 Length: 167
Score: 554.00 Matches: 106
Percent Similarity: 93.22% Conservative: 4
Best Local Similarity: 89.83% Mismatches: 6
Query Match: 79.60% Indels: 2
DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-472-087-80 (1-167)

QY      28  GGCGCTGGTCACGCGCTGGAGAGTCCCTGAGACTCTCCTGTGCAGCCTCTGATTCACCTTC      87
      1  G|YValValGlnInrProG|YArSerSerLeuArG|LeuSerCyAlaAla|SerGlyPheThrPhe  20
QY      88  AGTACTGATGGCATGCATCTGGGTCCGCCAGCGCTCCAGGCGTCAAGGGCGTGAAGTGGTGCA  14
      21  SerSerTyrlY|methIstR|PValA|G|GlnAla|ProG|Y|LysG|Y|LeuG|Inr|PValAla  40
QY     148  GTTATATCATATGATATGGAAGTAAATATCTATGACAGACTCCGTGAGAGGGCCGATTCACC  20
      41  Val|Le|rrP|Yr|Asp|G|Y|Ser|Leu|Yr|Yr|Ala|Asp|Ser|Val|G|Ala|Yr|G|He|Thr  60
Db      208  ATCTCCAGACAGCAATTCCAAGAAACACGCTGTATCTGCAATGACAACAGCCTGAGACTGAG  26
      61  I|SerArG|Asp|Sen|Ser|Lys|Asn|Thr|Leu|Yr|Leu|G|Met|Asn|Ser|Leu|ArG|Ala|G|U  80
QY     268  GACACGCGCTGTATTACTGTCTGGGAAGATATGAGGGGTGGGCGACGTGCGTGAAGACCTTAC  32
      81  Asph|Thr|Ala|Val|Yr|Yr|Cys|Ala|Asp|Pro|ArG|G|Y|Ala|Thr|Leu|Yr|----|Tyr  98
QY     328  TACTACTACGGTATGACGCTGTGGGCGCAAGGGACCAACGCGTCAACCGTCTCTCA  381
      99  Ty|Tyr|Tyr|G|Y|Met|Asp|Val|Trp|G|Y|G|In|G|Y|Thr|Thr|Val|Ser  116

RESULT 8
US-09-079-029-11
: Sequence 11, Application US/09079029
: Patent No. 6342369
: GENERAL INFORMATION:
: APPLICANT: Adams, Camilla W.
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Chuntcharapal, Anan
: APPLICANT: Kim, Kyung J.
: TITLE OF INVENTION: Apo-2 Receptor
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079,029
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1101R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 11:

```



```
SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-11

Alignment Scores:
Pred. No.: 1 036-54 Length: 310
Score: 553.50 Matches: 106
Percent Similarity: 88.19% Conservative: 6
Best Local Similarity: 83.46% Mismatches: 6
Query Match: 79.53% Indels: 9
DB: 3 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-079-029-11 (1-310)

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 40 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 59
QY 61 TCCTGTGAGCCTCTGAGATTCACTTCAGTACTTGGCATGCACTGGTCCGAGGCT 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 60 SerCysAlaAlaSerGlyPheLeuPheSerSerTyrglyMetHisTrpValArgGlnAla 79
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATATATATATATGAGTAATAATAACTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 80 ProGlyIysGlyLeuGlnTrpValAlaGlyIlePheTyraPspGlyGlyAsnLysTyrr 99
QY 181 GCAGACTCCGTAAGGGCGGATTCACATCTTCAGAGACAATTCAGAGACGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 100 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 119
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTGTATTCTGTGCGAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 120 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaArgAspArg 139
QY 301 GGGTGGGGCAGTGGCTGAGACCCCTACTACTAGGTAATGAGAGCTGCGGGCCCAAGG 360
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 140 Gly-----TyrTyrrTyrrMetAspValTrpGlyGln 150
QY 361 ACCAGCGTACCGTCTCTCA 381
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 151 ThrThrValThrValSerSer 157

RESULT 9
US-09-840-459-77
; Sequence 77, Application US/09840459
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
```

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ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) ... (128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77

Alignment Scores:
Pred. No.: 9,896-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-840-459-77 (1-128)

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyIysSerLeuArgLeu 20
QY 61 TCCTGTGAGCCTCTGAGATTCACTTCAGTACTTGGCATGCACTGGTCCGAGGCT 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATATATATATGAGTAATAATAACTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyIysGlyLeuGlnTrpValSerAlaIleSerIysSerGlyGlySerThrTyrr 60
QY 181 GCAGACTCCGTAAGGGCGGATTCACCATCTTCAGAGACAATTCAGAGACGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTGTATTCTGTGCGAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaArgAspArg 100
QY 301 GGGTGGGGCAGTGGCTGAGAC---CCCTACTACTACTAGGTAATGAGAGCTGCGGGCCCA 357
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 101 ArgAsnTyraPspPheTrpSerGly**TyrTyrrTyrrGlyMetAspValTrpGlyGln 120
QY 358 GGGACGACGGTACCGTCTCTCA 381
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 121 GlyThrThrValThrValSerSer 128

RESULT 10
US-09-840-459-79
; Sequence 79, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-403-107-143_COPY_1_381 (1-381) x US-09-840-459-79 (1-128)

Alignment Scores:
Pred. No.: 9.89e-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-840-459-79 (1-128)
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Db 1 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATTCACTTCAGTAGCTATGCAATGCACTGGTCCCGCAGGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrIaIaMetSerTrpValArgGlnIa 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAGTAAATACTAT 180
Db 41 ProGlyIyGlyLeuGlnTrpValSerAlaIaIaSerGlySerGlySerThrTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCGAGAGCAATTCAGAGACGCTGAT 240
Db 61 AlaAspSerValIySerGlyArgPheThrIleSerArgAspAsnSerIyAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaIyAspArg 100
QY 301 GGGTGGGGCAGTGGCTGGAGA---CCCTACTACTACAGGTATGAGCGTGGGGGCCAA 357
Db 101 ArgAsnTyrAspPheTrpSerGly**TyrTyrTyrTyrGlyMetAspValTrpGlyGln 120
QY 358 GGGACCAAGGCTCAACCGTCTCTCA 381
Db 121 GlyThrThrValThrValSerSer 128

RESULT 11
US-09-497-625A-77
; Sequence 77, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-497-625A-77

Alignment Scores:
Pred. No.: 9.89e-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-497-625A-77 (1-128)
QY 1 GAGGTGACGCTGCTGAGCTGGGGAGAGCGCTGAGCTGGAGAGTCCCTGAGACTC 60
Db 1 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATTCACTTCAGTAGCTATGCAATGCACTGGTCCCGCAGGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrIaIaMetSerTrpValArgGlnIa 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAGTAAATACTAT 180
Db 41 ProGlyIyGlyLeuGlnTrpValSerAlaIaIaSerGlySerGlySerThrTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCGAGAGCAATTCAGAGACGCTGAT 240
Db 61 AlaAspSerValIySerGlyArgPheThrIleSerArgAspAsnSerIyAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaIyAspArg 100
QY 301 GGGTGGGGCAGTGGCTGGAGA--CCCTACTACTACTACGATATGAGCGTGGGGGCCAA 357
Db 101 ArgAsnTyrAspPheTrpSerGly**TyrTyrTyrTyrGlyMetAspValTrpGlyGln 120
QY 358 GGGACCAAGGCTCAACCGTCTCTCA 381
Db 121 GlyThrThrValThrValSerSer 128

RESULT 12
US-09-497-625A-79
; Sequence 79, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
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US-09-497-625A-79

Alignment Scores:
 Pred. No.: 9, 89e-55 Length: 128
 Score: 552.50 Matches: 109
 Percent Similarity: 86.72% Conservative: 2
 Best Local Similarity: 85.16% Mismatches: 16
 Query Match: 79.38% Indels: 1
 DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-497-625A-79 (1-128)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCTGTGTCAGCTGGAGGTCCTGAGACTC 60
 DB 1 GIVVIGLNLNLEUIGLUSERGLYGLYGLNIPROGLYGLYSERLEUARGLEU 20
 QY 61 TCTGTGACGCTGCTGATTCACCTTACAGTATGAGTATGAGTATGAGTATG 120
 DB 21 SERCYSAIAAASERGLYPHERPHERSERGLYALAMETSERTRIPVALARGINLA 40
 QY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAAGTAAATACTAT 180
 DB 41 PROGLYVSGLYLNGLUTRIPVALSERALLESERGLYSERGLYSETHRTYR 60
 QY 181 GCAGACTCGGTGAGGGCCGATTCACTCTCAGAGCAATTCAGAGACGCTGTAT 240
 DB 61 AIAAPSERVALYGLYARGPHERTHRILESERARGAPASERLYASANTHRLTYR 80
 QY 241 CTGCAATGAAACAGCTGAGCTGAGACGACGCTGTGTATCTGTGCGAAGATATG 300
 DB 81 LEUGINMETAESERLEUARGALAGLUNAPHTHALAVALTYRTRYCYALALASAPARG 100
 QY 301 GGGTGGGACAGTGGCTGAGA---CCCTACTACTACTACGTATGAGAGCTGGGGCCAA 357
 DB 101 ARGANTYRASPHERTRIPSERGLY**TYRTRYRTRYRGLYMETASPVALTIPGLYGLN 120
 QY 358 GGGACACGAGTACCGTCTCCTCA 381
 DB 121 GLYTHRTVALTRVALSER 128

RESULT 13

US-09-240-274-140
 ; Sequence 140, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; FILE REFERENCE: 09596-4202
 ; CURRENT APPLICATION NUMBER: US/09/240,274
 ; EARLIER FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 140
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
 ; US-09-240-274-140

Alignment Scores:
 Pred. No.: 1.12e-54 Length: 125
 Score: 552.00 Matches: 106
 Percent Similarity: 90.55% Conservative: 9
 Best Local Similarity: 83.46% Mismatches: 10
 Query Match: 79.31% Indels: 2
 DB: 3 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-240-274-140 (1-125)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCTGTGTCAGCTGGAGGTCCTGAGACTC 60
 DB 1 GIVVIGLNLNLEUIGLUSERGLYGLYGLNIPROGLYGLYSERLEUARGLEU 20
 QY 61 TCTGTGACGCTGCTGATTCACCTTACAGTATGAGTATGAGTATGAGTATG 120
 DB 21 SERCYSAIAAASERGLYPHERPHERSERGLYALAMETSERTRIPVALARGINLA 40
 QY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAAGTAAATACTAT 180
 DB 41 PROGLYVSGLYLNGLUTRIPVALALALEULETTRIPVALYASANTHRLTYR 60
 QY 181 GCAGACTCGGTGAGGGCCGATTCACTCTCAGAGCAATTCAGAGACGCTGTAT 240
 DB 61 AIAAPSERVALYGLYARGPHERTHRILESERARGAPASERLYASANTHRLTYR 80
 QY 241 CTGCAATGAAACAGCTGAGCTGAGACGACGCTGTGTATCTGTGCGAAGATATG 300
 DB 81 LEUGINMETAESERLEUARGALAGLUNAPHTHALAVALTYRTRYCYALALASAPGLN 100
 QY 301 GGGTGGGACAGTGGCTGAGACCTACTACTACTACGTATGAGAGCTGGGGCCAA 360
 DB 101 ARGALALALAGLY-----LLEPHERTRYRTRYRGLYMETASPVALTIPGLYGLN 118
 QY 361 ACACGCTACCGTCTCCTCA 381
 DB 119 THRTRVALTRVALSER 125

RESULT 14

US-07-942-245-35
 ; Sequence 35, Application US/07942245
 ; Patent No. 5639641
 ; GENERAL INFORMATION:
 ; APPLICANT: PEDERSEN, Jan T.
 ; APPLICANT: REES, Anthony R.
 ; APPLICANT: ROGUSKA, Michael A.
 ; APPLICANT: GUID, Braydon C.
 ; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
 ; NUMBER OF SEQUENCES: 522
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
 ; STREET: 2100 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: United States
 ; ZIP: 20037-3202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: HP 9000/700 Workstation
 ; OPERATING SYSTEM: UNIX
 ; SOFTWARE: in house
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/942,245
 ; FILING DATE: 09-SEP-1992
 ; CLASSIFICATION: 530
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 293-7060
 ; TELEFAX: (202) 293-7860
 ; TELEX: 6491103
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-942-245-35

Alignment Scores:
 Pred. No.: 4.12e-54 Length: 120

Score: 547.00 Matches: 107
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Best Local Similarity: 82.95% Mismatches: 7
Query Match: 78.59% Indels: 12
DB: 1 Gaps: 2

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QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTATGTCATGCACTGGGTCCGCCAGGCT 120
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Db 21 SerCyAlaAlaSerGlyPheThrPheSerSerTyrAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGGAGTGGGTGGGCAATTATCATATGATGAAGTAATAATCTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCCAAGACAGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTTGAGAGCTGAGACACGCGTGTGTATTAATCTGTGCG----- 291
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspArg 100
QY 292 AAGATATGGGGTGGGGGCACTGGAGACCTACTACTACTACGTATGACGCTCTGG 351
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 101 LysAspTrpGlyTyrPheLeu-----PheAspTyrTrp 111
QY 352 GGCCAAAGGACACGCTACCGTCTCC 378
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Db 112 GlyGlnGlyThrLeuValThrValSer 120
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RESULT 15

US-09-560-198A-2

/ Sequence 2, Application US/09560198A

/ Patent No. 6492497

/ GENERAL INFORMATION:

/ APPLICANT: Thompson, Julia E

/ APPLICANT: Leonard, Simon N

/ APPLICANT: Wilton, Alison J

/ APPLICANT: Braddock, Peta SH

/ APPLICANT: Du Fou, Sarah L

/ APPLICANT: McCallerty, John G

/ APPLICANT: Conroy, Louise A

/ APPLICANT: Tempest, Philip R

/ TITLE OF INVENTION: Specific binding members for TGFbeta1

/ FILE REFERENCE: 28111/35620A

/ CURRENT APPLICATION NUMBER: US/09/560,198A

/ CURRENT FILING DATE: 2000-04-28

/ PRIOR APPLICATION NUMBER: US 60/131,983

/ PRIOR FILING DATE: 1999-04-30

/ NUMBER OF SEQ ID NOS: 25

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 2

/ LENGTH: 123

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-09-560-198A-2

Alignment Scores:

Pred. No.: 5,41e-54 Length: 123

Score: 546.00 Matches: 108

Percent Similarity: 91.34% Conservative: 8

Best Local Similarity: 85.04% Mismatches: 7

Query Match: 78.45% Indels: 4

DB: 4 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-09-560-198A-2 (1-123)

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QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTATGTCATGCACTGGGTCCGCCAGGCT 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGGAGTGGGTGGGCAATTATCATATGATGAAGTAATAATCTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerIleLysTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCCAAGACAGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTTGAGAGCTGAGACACGCGTGTGTATTAATCTGTGCG----- 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArg--Thr 99
QY 301 GGGTGGGCAAGTGGCTGAGAGACCTACTACTACTACGTATGATGAGGTCTGGGCAAGGG 360
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 100 GlyGlnTyrSerGly-----TyrAspThrSerGlyValGlnLeuTrpGlyGlnGly 116
QY 361 ACCACGGTCAACCGTCTCTCA 381
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GenCore version 5.1.6
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Fgapop 6.0 , Fgapext 7.0
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Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 3534298

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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22: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	98.6	138	US-10-325-694-150	Sequence 150, App
2	686	98.6	457	US-10-778-915-1	Sequence 1, Appl1
3	683	98.1	138	US-10-325-694-144	Sequence 144, App
4	612	87.9	127	US-10-706-689-22	Sequence 22, Appl1
5	612	87.9	127	US-10-988-360-22	Sequence 22, Appl1
6	608.5	87.4	124	US-10-371-942-82	Sequence 82, Appl1
7	608	87.4	127	US-10-706-689-36	Sequence 36, Appl1
8	608	87.4	127	US-10-988-360-36	Sequence 36, Appl1
9	602	86.5	125	US-10-292-088-107	Sequence 107, App
10	601	86.4	123	US-10-292-088-116	Sequence 116, App
11	598.5	86.0	122	US-09-144-886-68	Sequence 68, Appl1
12	598.5	86.0	122	US-10-632-706-65	Sequence 65, Appl1
13	597.5	85.8	122	US-09-144-886-69	Sequence 69, Appl1
14	597.5	85.8	122	US-10-632-706-66	Sequence 66, Appl1
15	597.5	85.8	122	US-10-727-155-34	Sequence 34, Appl1
16	597	85.8	122	US-10-292-088-115	Sequence 115, App
17	595.5	85.6	126	US-10-727-155-128	Sequence 128, App
18	595	85.5	123	US-10-292-088-117	Sequence 117, App
19	594.5	85.4	124	US-10-292-088-106	Sequence 106, App
20	591	84.9	451	US-10-153-382-17	Sequence 17, Appl1
21	591	84.9	451	US-10-612-497-70	Sequence 70, Appl1
22	591	84.9	451	US-10-776-649-70	Sequence 70, Appl1
23	590	84.8	123	US-10-269-711-43	Sequence 43, Appl1
24	590	84.8	123	US-10-684-109-35	Sequence 35, Appl1
25	589.5	84.7	126	US-10-041-860-282	Sequence 282, App
26	589.5	84.7	126	US-10-041-860-17	Sequence 17, Appl1
27	589.5	84.7	126	US-10-041-860-25	Sequence 25, Appl1
28	589.5	84.7	126	US-10-041-860-209	Sequence 209, App
29	589.5	84.7	126	US-10-041-860-210	Sequence 210, App
30	589.5	84.7	126	US-10-041-860-246	Sequence 246, App
31	589.5	84.7	126	US-10-041-860-282	Sequence 282, App
32	589.5	84.7	126	US-10-041-860-306	Sequence 306, App
33	589.5	84.7	126	US-10-665-383-14	Sequence 14, Appl1
34	589.5	84.7	134	US-10-665-383-30	Sequence 30, Appl1
35	587	84.3	123	US-10-727-155-254	Sequence 254, App
36	587	84.3	123	US-10-269-711-11	Sequence 11, Appl1
37	587	84.3	123	US-10-269-711-23	Sequence 23, Appl1
38	587	84.3	123	US-10-269-711-27	Sequence 27, Appl1
39	587	84.3	123	US-10-269-711-31	Sequence 31, Appl1
40	587	84.3	123	US-10-269-711-35	Sequence 35, Appl1
41	586	84.2	123	US-10-684-109-11	Sequence 11, Appl1
42	586	84.2	252	US-10-727-155-124	Sequence 124, Appl1
43	586	84.2	252	US-09-880-748-1731	Sequence 1731, App
44	585.5	84.1	141	US-10-293-418-1731	Sequence 1731, App
45	585.5	84.1	249	US-10-858-855-11	Sequence 11, Appl1
			10	US-09-880-748-512	Sequence 512, App

ALIGNMENTS

RESULT 1
US-10-325-694-150
Sequence 150, Application US/10325694
Publication No. US20030148463A1
GENERAL INFORMATION:
APPLICANT: KUFER, PETER
APPLICANT: RAMM, TOBIAS
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 150
LENGTH: 138
TYPE: PRT
ORGANISM: HUMAN

US-10-325-694-150

Alignment Scores:

Pred. No.: 1,68e-61 Length: 138
Score: 686.00 Matches: 126
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.21% Mismatches: 0
Query Match: 98.56% Indels: 0
DB: 14 Gaps: 0

US-09-403-107-143_COPY_1_381 (1-381) x US-10-325-694-150 (1-138)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTCAGAGCTGGAGGTCCCTGAGACTC 60
Db 1 G|UvAlG|InLeu|euG|InSer|G|Yg|Y|Val|AlG|InProG|I|Y|ArSer|Leu|ArG|Leu 20
QY 61 TCCTGTGACGCTCTGTGATTACCTTCAGTAGCTATGAGCATTCGAGTCCGCCAGGCT 120
Db 21 SerCyAlAlAlAserG|Y|Phe|Thr|Phe|Ser|Ser|Y|G|Y|Me|Ch|I|Str|P|Val|ArG|In|Al 40
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGATGGAAGTAAATAACTAT 180
Db 41 ProG|I|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGAACGCTGTAT 240
Db 61 AlAAspSerVal|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 80
QY 241 CTGCAATGAACAAGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGATANG 300
Db 81 LeuG|In|Me|Ar|S|er|Leu|ArG|Al|Al|Asp|Thr|Al|Al|Val|Y|Tr|Y|Cy|Sa|Al|Al|Y|S|Asp|Me|C 100
QY 301 GGGTGGGGCAGTGGCTGGAGAACCTTACTACTACGTATGACGTCGTGGGCCAAAGG 360
Db 101 G|Y|Tr|P|G|I|Y|Ser|G|I|Y|Tr|P|Ar|G|Pro|Y|Tr|Y|Tr|Y|G|Y|Me|C|Asp|Val|Tr|P|G|I|Y|InG|I|Y 120
QY 361 ACCACGGTCACCGTCTCTCA 381
Db 121 Thr|Thr|Val|Thr|Val|Ser|Ser 127

RESULT 2

US-10-778-915-1
; Sequence 1, Application US/10778915
; Publication No. US20050180979A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, MATTHEW
; APPLICANT: LOCHER, MATTHIAS
; APPLICANT: PRANG, NADJA
; APPLICANT: QUADT, CORNELIA
; TITLE OF INVENTION: Anti-EpCAM Immunoglobulins
; FILE REFERENCE: DEBR.031US
; CURRENT APPLICATION NUMBER: US/10/778,915
; CURRENT FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-778-915-1

Alignment Scores:

Pred. No.: 2,09e-61 Length: 457
Score: 686.00 Matches: 126
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.21% Mismatches: 0
Query Match: 98.56% Indels: 0
DB: 18 Gaps: 0

US-09-403-107-143_COPY_1_381 (1-381) x US-10-778-915-1 (1-457)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTCAGAGCTGGAGGTCCCTGAGACTC 60
Db 1 G|UvAlG|InLeu|euG|InSer|G|Yg|Y|Val|AlG|InProG|I|Y|ArSer|Leu|ArG|Leu 20
QY 61 TCCTGTGACGCTCTGTGATTACCTTCAGTAGCTATGAGCATTCGAGTCCGCCAGGCT 120
Db 21 SerCyAlAlAlAserG|Y|Phe|Thr|Phe|Ser|Ser|Y|G|Y|Me|Ch|I|Str|P|Val|ArG|In|Al 40
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGATGGAAGTAAATAACTAT 180
Db 41 ProG|I|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGAACGCTGTAT 240
Db 61 AlAAspSerVal|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 80
QY 241 CTGCAATGAACAAGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGATANG 300
Db 41 ProG|I|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 60
QY 301 GGGTGGGGCAGTGGCTGGAGAACCTTACTACTACGTATGACGTCGTGGGCCAAAGG 360
Db 101 G|Y|Tr|P|G|I|Y|Ser|G|I|Y|Tr|P|Ar|G|Pro|Y|Tr|Y|Tr|Y|G|Y|Me|C|Asp|Val|Tr|P|G|I|Y|InG|I|Y 120
QY 361 ACCACGGTCACCGTCTCTCA 381
Db 121 Thr|Thr|Val|Thr|Val|Ser|Ser 127

RESULT 3

US-10-325-694-144
; Sequence 144, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-144

Alignment Scores:

Pred. No.: 3,41e-61 Length: 138
Score: 683.00 Matches: 125
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.43% Mismatches: 0
Query Match: 98.13% Indels: 0
DB: 14 Gaps: 0

US-09-403-107-143_COPY_1_381 (1-381) x US-10-325-694-144 (1-138)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTCAGAGCTGGAGGTCCCTGAGACTC 60
Db 1 G|UvAlG|InLeu|Val|I|U|Ser|G|Yg|Y|Val|AlG|InProG|I|Y|ArSer|Leu|ArG|Leu 20
QY 61 TCCTGTGACGCTCTGTGATTACCTTCAGTAGCTATGAGCATTCGAGTCCGCCAGGCT 120
Db 21 SerCyAlAlAlAserG|Y|Phe|Thr|Phe|Ser|Ser|Y|G|Y|Me|Ch|I|Str|P|Val|ArG|In|Al 40
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGATGGAAGTAAATAACTAT 180
Db 41 ProG|I|Y|LeG|I|Y|LeuG|I|U|Tr|P|Val|Al|Al|Val|I|LeSer|Y|ArSpG|I|Y|Ser|Am|Y|Str|Y|Tr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGAACGCTGTAT 240

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Db 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGTGTGATTACTGTGCAAAATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaIleLysAspMet 100
Qy 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGCGTATGAGAGCTTGGGGCCAAAGG 360
Db 101 G1YTPG1YSerG1YTPArgProTyrTyrTyrG1YMetAspValTPG1YglnG1 120
Qy 361 ACCAGCGTCACTGCTCTCA 381
Db 121 ThrThrValThrValSerSer 127

RESULT 4
US-10-706-689-22
; Sequence 22, Application US/10706689
; Publication No. US20050100965A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-085
; CURRENT APPLICATION NUMBER: US/10/706,689
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-689-22

Alignment Scores:
Pred. No.: 6,49e-54 Length: 127
Score: 612.00 Matches: 115
Percent Similarity: 94.53% Conservative: 6
Best Local Similarity: 89.84% Mismatches: 5
Query Match: 87.93% Indels: 2
Gaps: 17

US-09-403-107-143_COPY_1_381 (1-381) x US-10-706-689-22 (1-127)
Qy 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGTCCAGCTGGAGGTCCTTGAGACTC 60
Db 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCCGTGAGGCTCTGAGTTCAGCTTCAGTAGCATTAGCAGCAGCAGCTGGTCCGACAGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerHisTyrGlyMetHisTyrValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATCATATGATGGAAGTAATAATACTAT 180
Db 41 ProGlyysGlyLeuGlnTyrValAlaValIleSerTyrAspGlyArgAsnLysTyrTyr 60
Qy 181 GCAAGCTCCGTGAAGGGCCGATTCACTTCACAGAGCAATTCAGAGACACGCTGTAT 240
Db 61 ValAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGTGTGATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValPheTyrCysAlaArgGlnLys 100
Qy 301 GGGTGGGGCAGTGGCTGAGAGACC--TACTACTACTACGCGTATGAGAGCTTGGGGCCAA 357
Db 101 Gly---GlySerGlyTyrProProPheTyrTyrTyrGlyMetAspValTPG1Ygln 119
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Qy 358 GGGACCAAGCTCACTCTCTCA 381
Db 120 G1YThrThrValThrValSerSer 127

RESULT 5
US-10-988-360-22
; Sequence 22, Application US/10988360
; Publication No. US20050147610A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-0850S
; CURRENT APPLICATION NUMBER: US/10/988,360
; CURRENT FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-988-360-22

Alignment Scores:
Pred. No.: 6,49e-54 Length: 127
Score: 612.00 Matches: 115
Percent Similarity: 94.53% Conservative: 6
Best Local Similarity: 89.84% Mismatches: 5
Query Match: 87.93% Indels: 2
Gaps: 18

US-09-403-107-143_COPY_1_381 (1-381) x US-10-988-360-22 (1-127)
Qy 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGTCCAGCTGGAGGTCCTTGAGACTC 60
Db 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCCGTGAGGCTCTGAGTTCAGCTTCAGTAGCATTAGCAGCAGCAGCTGGTCCGACAGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerHisTyrGlyMetHisTyrValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATCATATGATGGAAGTAATAATACTAT 180
Db 41 ProGlyysGlyLeuGlnTyrValAlaValIleSerTyrAspGlyArgAsnLysTyrTyr 60
Qy 181 GCAAGCTCCGTGAAGGGCCGATTCACTTCAGAGCAATTCAGAGACACGCTGTAT 240
Db 61 ValAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGTGTGATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValPheTyrCysAlaArgGlnLys 100
Qy 301 GGGTGGGGCAGTGGCTGAGAGACC--TACTACTACTACGCGTATGAGAGCTTGGGGCCAA 357
Db 101 Gly---GlySerGlyTyrProProPheTyrTyrTyrGlyMetAspValTPG1Ygln 119
Qy 358 GGGACCAAGCTCACTCTCTCA 381
Db 120 G1YThrThrValThrValSerSer 127

RESULT 6
US-10-371-942-82
; Sequence 82, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
```

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; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-371-942-82

Alignment Scores:
Pred. No.: 1.48e-53 Length: 124
Score: 608.50 Matches: 114
Percent Similarity: 94.49% Conservative: 6
Best Local Similarity: 89.76% Mismatches: 4
Query Match: 87.43% Indels: 3
DB: 15 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-10-371-942-82 (1-124)
QY 1 GAGGTGACAGTGTGTCAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTATGAGTATGAGTATGAGTATGAGTATG 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrcylMetHisTrpValAlaGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGCAATTATATGATATGATATGATATATATAT 180
DB 41 ProGlyLyseGlyLeuGluTrpValAlaValIleSerTyrcAspGlySerAsnIleuTy 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAAGACGCTGTAT 240
DB 61 AlaAspSerValIlysglyArgPheThrIleSerArgAspAsnSerIlyAsnThrLeuTy 80
QY 241 CTGCAATGAAACAGCCCTGAGAGCTGAGACACCGCTGTGTATTAATCTGTGCGAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIlyTyrcysAlaArgAspPhe 100
QY 301 GGGTGGGGCAGTGGCTGGAGACCCCTACTACTACTAGGATATGAGCTTGGGGCCAGGG 360
DB 101 AspTyrcIlyAspSer-----TyrcTyrcIlyTyrcIlyMetAspValTrpGlyGlnGly 117
QY 361 ACCAGGTCACGGTCTCCCTCA 381
DB 118 ThrThrValThrValSerSer 124

RESULT 7
US-10-706-689-36
; Sequence 36, Application US/10706689
; Publication No. US20050100965A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-085
; CURRENT APPLICATION NUMBER: US/10/706,689
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 47
```

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; SEQ ID NO 36
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-706-689-36

Alignment Scores:
Pred. No.: 1.67e-53 Length: 127
Score: 608.00 Matches: 118
Percent Similarity: 94.53% Conservative: 3
Best Local Similarity: 92.19% Mismatches: 5
Query Match: 87.36% Indels: 2
DB: 17 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-706-689-36 (1-127)
QY 1 GAGGTGACAGTGTGTCAGTCTGGGGAGGCGCTGTCAGCTGGAGGTCCCTGAGACTTC 60
DB 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTATGAGTATGAGTATGAGTATGAGTATG 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerHisCysGlyMetHisTrpValAlaGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGCAATTATATGATATGATATGATATATATATAT 180
DB 41 ProGlyLyseGlyLeuGluTrpValAlaValIleSerTyrcAspGlySerAsnIleuTy 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCGAAAGACGCTGTAT 240
DB 61 AlaAspSerValIlysglyArgPheThrIleSerArgAspAsnSerIlyAsnThrLeuTy 80
QY 241 CTGCAATGAAACAGCCCTGAGAGCTGAGACACCGCTGTGTATTAATCTGTGCGAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIlyTyrcysAlaArgAspHis 100
QY 301 GGGTGGGGCAGTGGCTGGAGACCC--TACTACTACTAGGATATGAGCTTGGGGCCAA 357
DB 101 Gly---GlySerGlySerProProPheTyrcIlyTyrcIlyMetAspValTrpGlyGln 119
QY 358 GGGACCAAGCTACCGTCTCCCTCA 381
DB 120 GlyThrThrValThrValSerSer 127

RESULT 8
US-10-988-360-36
; Sequence 36, Application US/10988360
; Publication No. US20050147610A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-085US
; CURRENT APPLICATION NUMBER: US/10/988,360
; CURRENT FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 36
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-988-360-36

Alignment Scores:
Pred. No.: 1.67e-53 Length: 127
Score: 608.00 Matches: 118
Percent Similarity: 94.53% Conservative: 3
```


Best Local Similarity: 92.19%
Query Match: 18
DB: 18

Mismatches: 5
Indels: 2
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-988-360-36 (1-127)

QY 1 GAGGTGACGCTGCTGAGCTGGGGGAGGCGCTGCTGAGGAGGCTCCCTGAGACTC 60
DB 1 +++ValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATTCACCTTCACTTCACTGAGCTATGAGCTAGCTGCTGCGCAGGCT 120
DB 21 SerGlyAlaAlaSerGlyPheThrPheSerHisGlyGlyMetHisTTPValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGAGTGGTGGCAGTTATATATATATATATATATATATATATAT 180
DB 41 ProGlyLysGlyLeuGlnTTPValAlaValIleSerTyrAspGlySerAsnLysTyr 60
QY 181 GCAGACTCCGTGAAAGGGCCGATTCACCTTCACTTCACTGAGCTATGAGCTATGAGCTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGAGCAGCTGATTAATTAATTAATTAATTAATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAspHis 100
QY 301 GAGTGGGCGAGTGGCTGAGAGCC--TACTACTACTACGCTATGAGAGCTGCGGCGCAA 357
DB 101 Gly---GlySerGlySerProProPheTyrTyrTyrTyrGlyMetAspValTTPGlyGln 119
QY 358 GGGACACGAGCTCACCGCTCTCTCA 381
DB 120 GlyThrThrValThrValSerSer 127

RESULT 9

US-10-292-088-107
; Sequence 107, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-107

Alignment Scores:

Pred. No.: 6,87e-53 Length: 125
Score: 602.00 Matches: 117
Percent Similarity: 95.28% Conservative: 4
Best Local Similarity: 92.13% Mismatches: 2
Query Match: 86.49% Indels: 4
DB: 15 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-292-088-107 (1-125)

QY 1 GAGGTGACGCTGCTGAGCTGGGGGAGGCGCTGCTGAGGAGGCTCCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATTCACCTTCACTTCACTGAGCTATGAGCTATGAGCTATGAGCTAT 180
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

DB 21 SerGlyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTTPValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGAGTGGTGGCAGTTATATATATATATATATATATATATATAT 180
DB 41 ProGlyLysGlyLeuGlnTTPValAlaValIleSerTyrAspGlySerAsnLysTyr 60
QY 181 GCAGACTCCGTGAAAGGGCCGATTCACCTTCACTTCACTGAGCTATGAGCTATGAGCTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGAGCAGCTGATTAATTAATTAATTAATTAATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLys--Met 99
QY 301 GAGTGGGCGAGTGGCTGAGAGCCCTTACTTACTTACTTACTTACTTACTTACTTACTT 360
DB 100 Gly---SerSerGlySerAspTyrTyrTyrTyrTyrGlyMetAspValTTPGlyGlnGly 118
QY 361 ACCACGCTCACCGTCTCTCTCA 381
DB 119 ThrThrValThrValSerSer 125

RESULT 10

US-10-292-088-116
; Sequence 116, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-116

Alignment Scores:
Pred. No.: 8.68e-53 Length: 123
Score: 601.00 Matches: 115
Percent Similarity: 95.28% Conservative: 6
Best Local Similarity: 90.55% Mismatches: 2
Query Match: 86.35% Indels: 4
DB: 15 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-292-088-116 (1-123)

QY 1 GAGGTGACGCTGCTGAGCTGGGGGAGGCGCTGCTGAGGAGGCTCCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGATTCACCTTCACTTCACTGAGCTATGAGCTAGCTGCTGCGCAGGCT 120
DB 21 SerGlyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTTPValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGAGTGGTGGCAGTTATATATATATATATATATATATATATAT 180
DB 41 ProGlyLysGlyLeuGlnTTPValAlaValIleSerTyrAspGlySerAsnLysTyr 60
QY 181 GCAGACTCCGTGAAAGGGCCGATTCACCTTCACTTCACTGAGCTATGAGCTATGAGCTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

QY	241	CTGCAAAATGAAKCGCCTGAGAGCTGAGCAACGGCTGCTGTTACTGTGCGAAAGATATG	300
Db	81	LeuGIImetamserIeuIauryaIaGIuIaaptIrrIaIaValIYrYrCYsAlaIaryasp---	99
QY	301	GGGGGGGGGAGGTGGCTGAGAACCCCTACTACTACTACGGATATGAGACGTGTGGGGCCAAAGGG	360
Db	100	---TyrIdIaAspTyrIYr-----IYrYrYrYrYrGIuIaetaspValIrrpGIyGIndIy	116
QY	361	ACCACGGTCAACGTCCTCTCTCA	381
Db	117	ThrThrValThrValaIserIser	123

```

RESULT 11
US-09-144-886-68
Sequence 68, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amerisdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ. ID NOS: 98
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 68
LENGTH: 122
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 1B3 region VH epitope 3
US-09-144-886-68

```

Alignment Scores:			
Pred. No.:	1,566-52	length:	122
Score:	598.50	Matches:	115
Percent Similarity:	92.13%	Conservative:	2
Best Local Similarity:	90.53%	Mismatches:	5
Query Match:	85.99%	Indels:	5
DB:	9	Gaps:	2
US-09-403-107-143_C00F1_381 (1-381)	x	US-09-144-886-68 (1-122)	

[illegible]

```

RESULT 12
US-10-632-706-65
; Sequence 65, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-65

```

Alignment Scores:	
Pred. No.:	1,56e-52
Score:	598.50
Percent Similarity:	92.13%
Best Local Similarity:	90.53%
Query Match:	85.99%
DB:	16
Length:	1222
Matches:	115
Conservative:	2
Mismatches:	5
Indels:	5
Gaps:	2

US-09-403-107-143 COPY 1 381 (1-381) X US-10-632-706-65 (1-122)

```

Oy      1  GAGGTGACGCTGCTCGAGTCGTGGGGGAGGCGCTGCTCCAGCCCTGGGAGGCTCCCTGAGACTC   60
Db      1  GlnValGlnIleuIndInuSerIlygIylValIaGlnProGlyArgSerIleuArgIleu   20
Oy      61  TCCGTGACGCTCTGGATTTCACCTTCAGTACTATGGCATGCACTCGAGTCCGCGAGGCT   120
Db      21  SerCyAlaIaIaSerIlypHeThrPheSerSerTyAlaIaMetHisTrpValArgGlnIla   40
Oy      121  CCAAGCGAAGGGGCTGAGTGGGTGGCGAGTTATATCATATGATGAGAGTAATAAATACTAT   180
Db      41  ProGlyIySerIyIeuGInuTrpValaIaValIleSerTyYrAspGlySerAsnIlyeTyTy   60
Oy      181  GCAGACTCTCGTGAAGGGCCGATTCCACCATCTCCAGAGACATTCGAAGAACAGCTGTAT   240
Db      61  AlaAspSerValIySerIlyArpHeThrIleSerArgAspAsnSerIyAsnThrIleuTy   80
Oy      241  CTGCAATATGAACGCTGAGAGGTGAGGACAGCGCGTGTATTACTGTGCGAAAGATATG   300
Db      81  LeuGlnMetSerIeuIeuArgIaGlnApIrrAlaValTyTyCyAlaIaArgAsp--   99
Oy      301  GGGGTGGGCGAGTGGCTGAGAGACCTTACTTACTTACGATAGSAGCTGGGGCCCAAGG   360
Db      100  ---TrpSerIndIy-----TyTyTyTyTyTyGlyMetAspValTrpGlyGlnIly   118
Oy      361  ACCACGGTCACCGCTCTCTCTCA   381
Db      116  ThrThrValIleValSerSer   122

RESULT 13
US-09-144-886-69
; Sequence 69, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins

```

```
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 69
LENGTH: 122
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-69

Alignment Scores:
Pred. No.: 1,98e-52 Length: 122
Score: 597.50 Matches: 113
Percent Similarity: 92.91% Conservative: 5
Best Local Similarity: 88.98% Mismatches: 4
Query Match: 85.85% Indels: 5
DB: 9 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-09-144-886-69 (1-122)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGGCTCCCTGAGACTC 60
DB 1 GlnIleGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCTGTGACGCTCTGATTCACCTTCAGTAGCTAGCATGACATGGGTCGCCAGGCT 120
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrlaMetHlstrpValArgGlnIla 40
QY 121 CCAGGCAAGGGGCTGAGAGTGGGTGGCACTTATATCATATGATGAAAGTAAATATACAT 180
DB 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrlaspGlySerAsnHlLeuTy 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrlTyCysAlaArgAsp--- 99
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACTACGTATGAGAGCTGTGGGGCCAGGG 360
DB 100 ---TtpSerGlnGly-----TyrlTyrlTyrlGlyMetAspValTrpGlyGlnGly 115
QY 361 ACCAGGTCACCGTCTCTCA 381
DB 116 ThrThrValIleValSerSer 122

RESULT 14
US-10-632-706-66
Sequence 66, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patent Version 3.2
SEQ ID NO 66
LENGTH: 122
TYPE: PRT
```

```
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-66

Alignment Scores:
Pred. No.: 1,98e-52 Length: 122
Score: 597.50 Matches: 113
Percent Similarity: 92.91% Conservative: 5
Best Local Similarity: 88.98% Mismatches: 4
Query Match: 85.85% Indels: 5
DB: 16 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-632-706-66 (1-122)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGGCTCCCTGAGACTC 60
DB 1 GlnIleGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCTGTGACGCTCTGATTCACCTTCAGTAGCTAGCATGACATGGGTCGCCAGGCT 120
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrlaMetHlstrpValArgGlnIla 40
QY 121 CCAGGCAAGGGGCTGAGAGTGGGTGGCACTTATATCATATGATGAAAGTAAATATACAT 180
DB 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrlaspGlySerAsnHlLeuTy 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGTATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrlTyCysAlaArgAsp--- 99
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACTACGTATGAGAGCTGTGGGGCCAGGG 360
DB 100 ---TtpSerGlnGly-----TyrlTyrlTyrlGlyMetAspValTrpGlyGlnGly 115
QY 361 ACCAGGTCACCGTCTCTCA 381
DB 116 ThrThrValIleValSerSer 122

RESULT 15
US-10-727-155-34
Sequence 34, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaapal S. Kang
APPLICANT: Orlit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendelcho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rosanne Lee
APPLICANT: Kathy Manchuliencho
APPLICANT: Raffaela Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: AGENIX. 073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
```

LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-34

Alignment Scores:

Pred. No.:	1.98e-52	Length:	122
Score:	597.50	Matches:	114
Percent Similarity:	92.91%	Conservative:	4
Best Local Similarity:	89.76%	Mismatches:	5
Query Match:	85.85%	Indels:	5
DB:	17	Gaps:	2

US-09-403-107-143_copy_1_381 (1-381) x US-10-727-155-34 (1-122)

```
QY      1 GAAGTGCAGCTGCTCGAGTCTGGGGAGGCTGTCACGCTGGGAGGTCCCTGAGACTC 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

QY      61 TCCTGTGACGCTCTGGATTCACTTCAGTAGCTATGGCATGGAGTGGGTCCGCCAGGCT 120
      |||
Db      21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40

QY      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGAAATAATAATCTAT 180
      |||
Db      41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60

QY      181 GCAGACTCCGCTGAAGGGCCGATTCACTATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
      |||
Db      61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

QY      241 CTGCAATGTAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGGCAAGATATG 300
      |||
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspGln 100

QY      301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGTATGACGTCTGGGGCCAAAGG 360
      |||
Db      101 -----AspAsnTrpAsn-----TyrTyrTyrGlyMetAspValTrpGlyGlnGly 115

QY      361 ACCACGGTCAACCGTCTCTCTCA 381
      |||
Db      116 ThrThrValThrValSerSer 122
```

Search completed: August 29, 2005, 11:30:07
Job time : 358.577 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 17.0962 Seconds

(without alignments)
4288.519 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381

Perfect score: 696
Sequence: 1 gaggtgcagctgcctgcagtc.....ccaggtaccgtctctcca 381

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US09403107/runat.29082005.120125.18902/app_query.fasta_1.1038
-DB=PIR -QFMT=fastan -SUFFIX=trpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=humand0.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09403107@cgn_1_1_77@runat.29082005.120125.18902 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594.5	85.4	128	2	S48797 Ig heavy chain V r
2	585.5	84.1	122	2	E36005 Ig heavy chain V r
3	587.5	83.7	147	2	I37780 Ig variable region
4	580	83.3	122	2	S31119 Ig heavy chain - h
5	572	82.2	123	2	S38493 Ig heavy chain - h
6	563	80.9	131	2	S19666 Ig heavy chain V r
7	562	80.7	132	2	S1603 Ig heavy chain V r
8	553.5	79.5	114	2	S46390 Ig heavy chain V r
9	553.5	79.5	118	2	S31116 Ig heavy chain - h
10	551	79.2	121	2	G36005 Ig heavy chain V r
11	548.5	78.8	122	2	S31117 Ig heavy chain - h
12	545	78.3	119	2	F36005 Ig heavy chain V r
13	543	78.0	130	2	PI0098 Ig heavy chain pre
14	542	77.9	160	2	S05271 Ig heavy chain pre

15	540.5	77.7	139	2	S31674 Ig heavy chain V r
16	539.5	77.5	114	2	S46392 Ig heavy chain V r
17	537	77.2	119	2	C36005 Ig heavy chain V r
18	536	77.0	130	2	S31601 Ig heavy chain V r
19	535	76.9	134	2	S31679 Ig heavy chain V r
20	534.5	76.8	137	2	S31701 Ig heavy chain V r
21	532	76.4	125	2	S37455 Ig mu chain - huma
22	530.5	76.2	140	2	S70442 Ig heavy chain pre
23	529.5	76.1	120	2	S31112 Ig heavy chain - h
24	528	75.9	135	2	S31598 Ig heavy chain V r
25	527.5	75.8	114	2	S46391 Ig heavy chain V r
26	525	75.4	111	2	PH1643 Ig heavy chain V r
27	525	75.4	133	2	A49028 Ig heavy chain V-I
28	523.5	75.2	120	2	S48798 Ig heavy chain V r
29	523	75.1	109	2	PH1644 Ig heavy chain V r
30	521.5	74.9	118	2	PH1660 Ig heavy chain V r
31	521.5	74.9	122	1	M3HDM Ig heavy chain V-I
32	519	74.6	121	2	S31104 Ig heavy chain (su
33	518	74.4	121	2	PH1661 Ig heavy chain V r
34	516.5	74.2	108	2	PH1642 Ig heavy chain V r
35	515	74.0	111	2	PH1645 Ig heavy chain V r
36	515	74.0	123	2	S26794 Ig heavy chain V r
37	513	73.7	109	2	PH1646 Ig heavy chain V r
38	513	73.7	113	2	S38490 Ig heavy chain - h
39	511.5	73.5	119	2	S31111 Ig heavy chain - h
40	511	73.4	117	2	S36270 Ig heavy chain V r
41	510	73.3	119	2	S31107 Ig heavy chain - h
42	509.5	73.2	151	2	A60943 Ig heavy chain pre
43	507	72.8	117	2	S36259 Ig heavy chain V r
44	507	72.8	119	2	D36005 Ig heavy chain V r
45	506.5	72.8	110	2	PH1655 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S48797 Ig heavy chain V region (anti-Sm, VH3/Dxp4/Oh6) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999

C/Accession: S48797; S26893

R/Matmoudi, M.; Edwards, J.; Cairns, B.; Bell, D.

submitted to the EMBL Data Library, October 1994

A/Description: Molecular characterization of natural human anti-Sm autoantibodies.

A/Reference number: S48797

A/Accession: S48797

A/Molecule type: mRNA

A/Residues: 1-128 <TM>

A/Cross-references: EMBL:Z12350; NID:g587147; PIDN:CAA86512.1; PID:g1340168

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/15-98/Domain: immunoglobulin homology <Im>

Alignment Scores:

Pred. No.: 2.03e-48

Score: 594.50

Percent Similarity: 93.80%

Best Local Similarity: 89.15%

Query Match: 85.42%

DB: 2

US-09-403-107-143_COPY_1_381 (1-381) x S48797 (1-128)

QY 1 GAGGTGAGCTGCTGAGTCTGGGGAGAGCTGGTCAAGCTGAGAGTCCCTGAGACTC 60

...|||||...|||||...|||||...|||||...|||||...|||||...|||||...|||||

```
Dh 1 GluValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCTGTGACACCTCTGTGATTACCTTCAGTAGCTAAGCATGACATGGGTCCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerSerGlyMetHisrTpValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGTGGCAGGTATATCATATATGAAATATAATAACTAT 180
Db 41 ProGlyLysGlyLeuGlnUTrPValAlaValIleTrpTyrAspIlySerAnlySrTyTy 60
Qy 181 GCAGACTCCGTGAAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAAACCGCTGTAT 240
Db 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAnThrLeuTy 80
Qy 241 CTGCAATATGAACCGCTGAGAGAGTGAAGACCGCTGTGTATATCTGTGCAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTyTyCysAlaArgAspAsn 100
Qy 301 GGGTGG-----GGACGTGGCTGGAGACCTACTACTACTACGTATGACGTGGGGC 354
Db 101 TyTrTyTrAspSerSerGlyTyTyTy---TyTrTyTyTrGlyMetAspValTrpGly 119
Qy 355 CAAGGACCAACGGTCAACCGTCTCTCTCA 381
Db 120 GlnGlyThrThrValThrValSerSer 128
```

RESULT 2

```
E36005
Ig heavy chain V region (M72) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: E36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: E36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-122 <SCH>
A/Cross-references: GB:M34030
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterocyclamer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
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Alignment Scores:

Pred. No.:	1,46e-47	Length:	122
Score:	585.50	Matches:	113
Percent Similarity:	92.13%	Conservative:	4
Best Local Similarity:	88.98%	Mismatches:	5
Query Match:	84.12%	Indels:	5
		Gaps:	2

US-09-403-107-143_COPY_1_381 (1-381) x E36005 (1-122)

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Qy 1 GAGGTGACAGTCTGTCAGTCTGGGGAGGCGCTGATCCAGCTGGAGGTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCTGTGACACCTCTGTGATTACCTTCAGTAGCTAAGCATGACATGGGTCCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerSerGlyMetHisrTpValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGTGGCAGGTATATCATATATGAAATATAATAACTAT 180
Db 41 ProGlyLysGlyLeuGlnUTrPValAlaValIleSerTyAspIlySerAnlySrTyTy 60
Qy 181 GCAGACTCCGTGAAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAAACCGCTGTAT 240
Db 120 GlnGlyThrThrValThrValSerSer
```

```
Dh 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAnThrLeuTy 80
Qy 241 CTGCAATATGAACCGCTGAGAGAGTGAAGACCGCTGTGTATATCTGTGCAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTyTyCysAlaArgAspArg 100
Qy 301 GGGTGGGCAAGGGGCTGAGACCTACTACTACTACGTATGACAGTCTGGGGCCAGGG 360
Db 101 ---HisSerSerTrp-----TyTrTyGlyMetAspValTrpGlyGlnGly 115
Qy 361 ACCACGCTCACCGTCTCTCTCA 381
Db 116 ThrThrValThrValSerSer 122
```

RESULT 3

```
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C/Accession: I37780; S25474
R/Demaison, C.; Chastagner, P.; These, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A/Title: Somatic diversification in the heavy chain variable region genes expressed by in
A/Reference number: A36876; MUID:94119917; PMID:8290556
A/Accession: I37780
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <RES>
A/Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/28-111/Domain: immunoglobulin homology <IMM>
```

Alignment Scores:

Pred. No.:	2,79e-47	Length:	147
Score:	582.50	Matches:	113
Percent Similarity:	89.76%	Conservative:	1
Best Local Similarity:	88.98%	Mismatches:	10
Query Match:	83.69%	Indels:	3
		Gaps:	1

US-09-403-107-143_COPY_1_381 (1-381) x I37780 (1-147)

```
Qy 1 GAGGTGACAGTCTGTCAGTCTGGGGAGGCGCTGATCCAGCTGGAGGTCCCTGAGACTC 60
Db 14 GluValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 33
Qy 61 TCTGTGACACCTCTGTGATTACCTTCAGTAGCTAAGCATGACATGGGTCCGCCAGGCT 120
Db 34 SerCysAlaIaSerGlyPheThrPheSerSerTyTrpMetSerTrpValArgGlnAla 53
Qy 121 CCAGGCAAGGGGCTGAGTGGTGGCAGGTATATCATATATGAAATATAACTAT 180
Db 54 ProGlyLysGlyLeuGlnUTrPValAlaValIleSerTyAspIlySerAnlySrTyTy 73
Qy 181 GCAGACTCCGTGAAGGGCCGATTCCACCATCTCCAGAGACAATTCAGAAACCGCTGTAT 240
Db 74 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAnThrLeuTy 93
Qy 241 CTGCAATATGAACCGCTGAGAGAGTGAAGACCGCTGTGTATATCTGTGCAAGATATG 300
Db 94 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTyTyCysAlaArgAsp 112
Qy 301 GGGTGGGCAAGGGGCTGAGACCTACTACTACTACGTATGACAGTCTGGGGCCAGGG 360
Db 113 -----GlyGlnGlyTrpGlyLeuTyTyTyTyTyGlyMetAspValTrpGlyGlnGly 130
Qy 361 ACCACGCTCACCGTCTCTCTCA 381
Db 131 ThrThrValThrValSerSer 137
```

RESULT 4

```
S31119
Ig heavy chain - human
```

```

Alignment Scores:
Pred. No.: 2.78e-46 Length: 123
Score: 572.00 Matches: 111
Percent Similarity: 90.55% Conservative: 4
Best Local Similarity: 87.40% Mismatches: 8
Query Match: 82.18% Indels: 4
DB: 2 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x S38493 (1-123)
QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGGTCAGCGCTGGAGAGTCCCTGAGATC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValGlnLeuGlnGlnSerGlyGlyValValGlnProGlyArgSerLeuSerLeu 20
   61 TCCTGTGACGCTCTGAGATTACCTTCAGTAGCTATGACATGCACTGGGCTGGCAGGCT 120
QY 21 SerGlyAlaIleSerGlyPheThrPheSerSerTyAlaMetHisTrpValArgGlnAla 40
   121 CCAGGCAAGGGGCTGAGAGTGGGTGGCGAGTTATTCATATGATGAAAGTAAATATCTAT 180
Db 41 ProGlyIysGlyLeuGlnTrpValAlaValIleSerTyArgPheIysSerAsnLysTrpTy 60
QY 181 GCGACATCCGTGAAGGGCGCATTCACCATCTCCAGAGACAAATTCGAAGAACAGCGTGTAT 240
   |||||||
Db 61 AlaAspSerValIysGlyArgPheThrIleSerTyArgAspAsnSerLysAsnTrpLeuTy 80
QY 241 CTCGCAATGAACAGCGCTGAGAGCTGAGAGACACGCGCTGTGATTACTGTGCCAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetSerAsnSerLeuArgAlaGlnAspThrAlaValTyTrpCyAsnAlaArgAlaArg 100
QY 301 GGGTGGGGCAGTGGCTGAGAGACCCCTACTACTACTACGATATGGACGCTTGGGGCCAAAGG 360
   |||||
Db 101 -----SerAsnTrpAsn---TyTrpTyTrpTyTrpMetAspValTrpGlyLysGly 116
QY 361 ACCACGGTCAACCGTCTTCCTCA 381
   |||||||
Db 117 ThrThrValThrValSerSer 123

RESULT 6
S19666
Ig heavy chain V region (VH3DHH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #ext_change 20-Jun-2000
C:Accession: S19666
R:Markers, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; WVID:92085276; PMID:1748994
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <NMR>
C:Cross-references: EMBL:X61646; NID:g37688; PIDD:CA443827.1; PIDD:g1335369
C:Superfamily: Immunoglobulin V region; Immunoglobulin Homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.99e-45 Length: 121
Score: 563.00 Matches: 110
Percent Similarity: 91.34% Conservative: 6
Best Local Similarity: 86.61% Mismatches: 5
Query Match: 80.89% Indels: 6
DB: 2 Gaps: 3

US-09-403-107-143_COPY_1_381 (1-381) x S19666 (1-121)
QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGGTCAGCGCTGGAGAGTCCCTGAGATC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
   61 TCCTGTGACGCTCTGAGATTACCTTCAGTAGCTATGACATGCACTGGGCTGGCAGGCT 120
QY 121 CCAGGCAAGGGGCTGAGAGTGGGTGGCGAGTTATTCATATGATGAAAGTAAATATCTAT 180
   |||||||
Db 121 SerGlyAlaIleSerGlyPheThrPheSerSerTyAlaMetHisTrpValArgGlnAla 40
   181 GCGACATCCGTGAAGGGCGCATTCACCATCTCCAGAGACAAATTCGAAGAACAGCGTGTAT 240
   |||||||
Db 181 AlaAspSerValIysGlyArgPheThrIleSerTyArgAspAsnSerLysAsnTrpLeuTy 80
QY 241 CTCGCAATGAACAGCGCTGAGAGCTGAGAGACACGCGCTGTGATTACTGTGCCAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 241 LeuGlnMetSerAsnSerLeuArgAlaGlnAspThrAlaValTyTrpCyAsnAlaArgAlaArg 100
QY 301 GGGTGGGGCAGTGGCTGAGAGACCCCTACTACTACTACGATATGGACGCTTGGGGCCAAAGG 360
   |||||
Db 301 -----SerAsnTrpAsn---TyTrpTyTrpTyTrpMetAspValTrpGlyLysGly 116
QY 361 ACCACGGTCAACCGTCTTCCTCA 381
   |||||||
Db 361 ThrThrValThrValSerSer 123

```

```
Dh 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrlYmethIstrValArgGlnAla 40
Qy 121 CCAAGGCAAGGGGCTGGAGTGGGGTGGCGAGTTATATCATATGATGAGATTAATACTAT 180
Db 41 ProGlyIysGlyLeuGluTrpValAlaValIleSerTyraSpGlySerAsnLysTyTyTy 60
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTAT 240
Db 61 AlaAspSerValIysGlyArgPheThrIleSerThrAspAsnSerLysAsnThrLeuTy 80
Qy 241 CTGCAATGAACAGCCTGAGAGCTGAGAGACAGCGCTGTATTACTGTGGCAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTyTyCysAlaLys---Thr 99
Qy 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACGCTATGACCGTCTGGGCGCAAGGG 360
Db 100 GlyTySerSerGlyTrpGly-----TyrPhe-----AspTyTrpGlyGlnGly 114
Qy 361 ACCACGGTCACCGCTCTCTCA 381
Db 115 ThrLeuValThrValSerSer 121
```

RESULT 7

S31603

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31603

R/CuiSinder, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <CUI>

A/Cross-references: EMBL:Z14168; NID:G30999; PIDN:CAA78537.1; PID:G31000

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:30-113/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2,47e-45	Length:	132
Score:	562.00	Matches:	108
Percent Similarity:	89.76%	Conservative:	6
Best Local Similarity:	85.04%	Mismatches:	3
Query Match:	80.75%	Indels:	10
DB:	2	Gaps:	2

US-09-403-107-143_COPY_1_381 (1-381) x S31603 (1-132)

```
Qy 1 GAGGTGACGCTGCTCCGAGTCTGGGGGAGCGCTGTCACAGCTCGGAGGTCCCTGAGACTC 60
Db 16 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyAspSerLeuArgLeu 35
Qy 61 TCCGTGACAGCCTCTGATTCACCTTCAGTAGTATGAGCATGAGCTGGTCCGCGAGCT 120
Db 36 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrlYmethIstrValArgGlnAla 55
Qy 121 CCAAGGCAAGGGGCTGAGTGGGGTGGCGATTATATCATATGAGTAATAATACTAT 180
Db 56 ProGlyIysGlyLeuGluTrpValAlaValIleSerTyraSpGlySerAsnLysTyTyTy 75
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTAT 240
Db 76 AlaAspSerValIysGlyArgPheThrIleSerThrAspAsnSerLysAsnThrLeuTy 95
Qy 241 CTGCAATGAACAGCCTGAGAGCTGAGAGACAGCGCTGTATTACTGTGGCAAGATATG 300
Db 96 LeuGlnMetAsnGlyLeuArgAlaGluAspThrAlaValTyTyTyCysAlaLysAspLeu 115
Qy 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACTACGCTATGACGCTGGGCGCAAGGG 360
Db 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACTACGCTATGACGCTGGGCGCAAGGG 360
```

```
Dh 116 -----PheTyTyTyPhe-----AspTyTrpGlyGlnGly 125
Qy 361 ACCACGGTCACCGCTCTCTCA 381
Db 126 ThrLeuValThrValSerSer 132
```

RESULT 8

S46390

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46390

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A/Reference number: S46390; MID:94254092; PMID:8196048

A/Accession: S46390

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <FIG>

A/Cross-references: EMBL:Z31686; NID:G509782; PIDN:CAA83491.1; PID:G1335143

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1,59e-44	Length:	114
Score:	553.50	Matches:	108
Percent Similarity:	87.40%	Conservative:	3
Best Local Similarity:	85.04%	Mismatches:	3
Query Match:	79.53%	Indels:	13
DB:	2	Gaps:	2

US-09-403-107-143_COPY_1_381 (1-381) x S46390 (1-114)

```
Qy 1 GAGGTGACGCTGCTCCGAGTCTGGGGGAGCGCTGTCACAGCTCGGAGGTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyAspSerLeuArgLeu 20
Qy 61 TCCGTGACAGCCTCTGATTCACCTTCAGTAGTATGAGCATGAGCTGGTCCGCGAGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrlYmethIstrValArgGlnAla 40
Qy 121 CCAAGGCAAGGGGCTGAGTGGGGTGGCGATTATATCATATGAGTAATAATACTAT 180
Db 41 ProGlyIysGlyLeuGluTrpValAlaValIleSerTyraSpGlySerAsnLysTyTyTy 60
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACAGCTGTAT 240
Db 61 AlaAspSerValIysGlyArgPheThrIleSerThrAspAsnSerLysAsnThrLeuTy 80
Qy 241 CTGCAATGAACAGCCTGAGAGCTGAGAGACAGCGCTGTATTACTGTGGCAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTyTyCysAlaLysAsp 99
Qy 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACTACGCTATGAGCATGAGCTGGGCGCAAGGG 360
Db 100 ---TrrpGly-----AspTyTrpGlyGlnGly 107
Qy 361 ACCACGGTCACCGCTCTCTCA 381
Db 108 ThrLeuValThrValSerSer 114
```

RESULT 9

S31116

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C/Accession: S31116

R/Naapfort, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme

A/Reference number: S31104; MID:92111633; PMID:1730252


```
QY 121 CCAGGCAAGGGGCTGAGTGGGCGACGTTATATCATATGATGAATAATACTAT 180
|||
Db 41 ProGlyLysGlyLeuGluTrpValAlaValIleTrpYrAspGlySerAsnLysTrpYr 60
|||
QY 181 GCAGACTCCGCTGGAAGGCGCATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
|||
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTrp 80
|||
QY 241 CTCGAATGAACAGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300
|||
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValLysTrpCysAlaArgAspPhe 100
|||
QY 301 GGGTGGGCGAGTGGCTGAGAACCCCTACTACTACTAGCGTATGACGCTGGGCGCAAGG 360
|||
Db 101 PheAlaProAsnTrpSerHisPhe-----AspTrpTrpGlyGlnGly 115
|||
QY 361 ACCACGCTCACCGCTCTCTCA 381
|||
Db 116 ThrLeuValThrValSerSer 122
|||
RESULT 12
F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C/Accession: F36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: F36005
A:Status: preliminary
A:Residues: 1-119 <SCH>
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; GB:M34026
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 1.02e-43 Length: 119
Score: 545.00 Matches: 105
Percent Similarity: 87.40% Conservative: 6
Best Local Similarity: 82.68% Mismatches: 8
Query Match: 78.30% Indels: 8
Gaps: 1
DB: 2
US-09-403-107-143_COPY_1_381 (1-381) x F36005 (1-119)
QY 1 GAGGTGAGTGTGCTGAGTGTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTC 60
|||
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
|||
QY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCGAGCT 120
|||
Db 21 SerCysAlaIleSerGlyPheThrPheSerSerTrpAlaMetHisTrpValArgGlnAla 40
|||
QY 121 CCAGGCAAGGGGCTGAGTGGGCGACGTTATATCATATGATGAATAATACTAT 180
|||
Db 41 ProGlyLysGlyLeuGluTrpValAlaValIleSerArgAspAsnSerLysAsnLysTrpYr 60
|||
QY 181 GCAGACTCCGCTGGAAGGCGCATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
|||
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTrp 80
|||
QY 241 CTCGAATGAACAGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300
|||
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValLysTrpCysAlaArgAspArg 100
|||
```

```
QY 301 GGGTGGGCGAGTGGCTGAGAACCCCTACTACTACTAGCGTATGAGCGTGGGCGCAAGG 360
|||
Db 101 LysAlaSerAspAlaPhe-----AspIleTrpGlyGlnGly 112
|||
QY 361 ACCACGCTCACCGCTCTCTCA 381
|||
Db 113 ThrMetValThrValSerSer 119
|||
RESULT 13
PL0098
Ig heavy chain precursor V-III region (FL2-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: PL0098
R/Nickerson, K.G.; Berman, J.; Glickman, E.; Cheese, L.; Alt, F.W.
J. Exp. Med. 169, 1391-1403, 1989
A:Title: Early human IGH gene assembly in Epstein-Barr virus-transformed fetal B cell
A:Reference number: PL0098; MUID:89176893; PMID:2538551
A:Accession: PL0098
A:Molecule type: DNA
A:Residues: 1-130 <NIC>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:17-110/Product: Ig heavy chain V-III region FL2-2 #status predicted <MAT>
F:32-115/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 1.57e-43 Length: 130
Score: 543.00 Matches: 104
Percent Similarity: 86.99% Conservative: 3
Best Local Similarity: 84.55% Mismatches: 6
Query Match: 78.02% Indels: 10
Gaps: 1
DB: 2
US-09-403-107-143_COPY_1_381 (1-381) x PL0098 (1-130)
QY 1 GAGGTGAGTGTGCTGAGTGTGGGGAGGCGCTGGTCCAGCTGGAGAGTCCCTGAGACTC 60
|||
Db 18 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 37
|||
QY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCGAGCT 120
|||
Db 38 SerCysAlaIleSerGlyPheThrPheSerSerTrpAlaMetHisTrpValArgGlnAla 57
|||
QY 121 CCAGGCAAGGGGCTGAGTGGGCGACGTTATATCATATGATGAATAATACTAT 180
|||
Db 58 LeuGlyLysGlyLeuGluTrpValAlaValIleSerTrpAspGlySerAsnLysTrpYr 77
|||
QY 181 GCAGACTCCGCTGGAAGGCGCATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240
|||
Db 78 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTrp 97
|||
QY 241 CTCGAATGAACAGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300
|||
Db 98 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValLysTrpCysAlaArgAspArg 117
|||
QY 301 GGGTGGGCGAGTGGCTGAGAACCCCTACTACTACTAGCGTATGAGCGTGGGCGCAAGG 360
|||
Db 118 AsnTrp-----GlyPheAspTrpTrpGlyGlnGly 127
|||
QY 361 ACCACGCTC 369
|||
Db 128 ThrLeuVal 130
|||
RESULT 14
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S05271; S04602
```

R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: EMBL:X14584
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1,94e-43 Length: 160
Score: 542.00 Matches: 107
Percent Similarity: 87.40% Conservative: 4
Best Local Similarity: 84.25% Mismatches: 14
Query Match: 77.87% Indels: 2
DB: Gaps: 1
Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x S05271 (1-160)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGCCCTGCTCCAGCCTGGAGGTCCCTGAGACTC 60
DB 20 GlnValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
QY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGACATGCGGCTCCGACGCT 120
DB 40 SerCysAlaAlaSerGlyPheThrPheSerThrTyraIleMetSerTrpValArgGlnAla 59
QY 121 CCAGGCAAGGGGCTGAGTGGGCTGAGCTTATATCATATGATGAGATTAATAATACTAT 180
DB 60 ProGlyLysGlyLeuGlnTrpValSerAlaIleSerGlySerGlySerThrTyrr 79
QY 181 GCAGACTCCGTGAAGGCGCATTCCTCCAGACCAATTCGAAGAACCGCTGAT 240
DB 80 AlaPseValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 99
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAGAATATG 300
DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaLysAlaVal 119
QY 301 GGGTGGGCGAGTGGTGAAGACCTTACTACTAGATGAGATGAGATGAGGCGGCGG 360
DB 120 -----ValArgGlyValIleSerTyrrTyrrTyrrGlyMetAspValTrpGlyGlnGly 137
QY 361 ACCAGGTCACCGCTCTCTCA 381
DB 138 ThrThrValThrValSerSer 144

RESULT 15
S31674
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31674
R:Cuisinier, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tomelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31674
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CUI>

A:Cross-references: EMBL:Z14204; NID:G30967; PIDN:CA478573.1; PID:G30968
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,71e-43 Length: 139
Score: 540.50 Matches: 107
Percent Similarity: 88.19% Conservative: 5
Best Local Similarity: 84.25% Mismatches: 8
Query Match: 77.66% Indels: 7
DB: Gaps: 2
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x S31674 (1-139)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGCCCTGCTCCAGCCTGGAGGTCCCTGAGACTC 60
DB 20 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 39
QY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGACATGCGGCTCCGACGCT 120
DB 40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrrGlyMetHsTrpValArgGlnAla 59
QY 121 CCAGGCAAGGGGCTGAGTGGGCTGAGCTTATATCATATGATGAGATTAATAATACTAT 180
DB 60 ProCysLysGlyLeuGlnTrpValAlaValIleSerTyrrAspLysSerAsnLysTyrr 79
QY 181 GCAGACTCCGTGAAGGCGCATTCACCATCTCCAGACCAATTCGAAGAACCGCTGAT 240
DB 80 AlaPseValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 99
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAGAATATG 300
DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaLys---Ala 118
QY 301 GGGTGGGCGAGTGGTGAAGACCTTACTACTAGATGAGATGAGATGAGGCGGCGG 360
DB 119 GlyLeuGly-----PhePheAsnTrpPheAspProTrpGlyGlnGly 132
QY 361 ACCAGGTCACCGCTCTCTCA 381
DB 133 ThrLeuValThrValSerSer 139

Search completed: August 29, 2005, 11:31:16
Job time : 19.0962 secs

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RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; AAH20240.1; -
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1645; PH1645.
DR PIR: PH1646; PH1646.
DR PIR: PLO098; PLO098.
DR PIR: PLO120; PLO120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSSP: P01861; 1ADQ.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG LIKE; 5.
DR PROSITE: PS00290; IG MHC; UNKNOWN; 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671B315 CRC64;

Alignment Scores:
Pred. No.: 4.09e-49 Length: 613
Score: 565.50 Matches: 109
Percent Similarity: 89.76% Conservative: 5
Best Local Similarity: 85.83% Mismatches: 6
Query Match: 81.25% Indels: 7
DB: 2 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x 08WUK1 (1-613)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCACGCTGGAGAGTCCCTGAGACTC 60
Db 20 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 39
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGACGTGGTCCGACGCT 120
Db 40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 59
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCGAGTATATCATATGATGAAATTAATAACTAT 180
Db 60 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 79
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCAGAAACAGCTGTAT 240
Db 80 AlaAspSerValLysGlyArgPheThrIleSerThrGAspAsnSerLysAsnThrLeuTyr 99
QY 241 CTGCAATGAACAGCGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300
Db 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAsp--- 118
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTACTACGATGAGCGTCTGGGGCCAAAGG 360
Db 119 ---TTPserGlnGlyValGlnTrpPhe-----AspIleTrpGlyGlnGly 132
QY 361 ACCACGGTACCGCTCTCTCA 381
Db 133 ThrMetValThrValSerSer 139

RESULT 2
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PSS0835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Alignment Scores:
Pred. No.: 2.21e-47 Length: 240
Score: 548.00 Matches: 106
Percent Similarity: 88.19% Conservative: 6
Best Local Similarity: 83.46% Mismatches: 5
Query Match: 78.74% Indels: 10
DB: 2 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x Q65ZC9 (1-240)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCACGCTGGAGAGTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGACGTGGTCCGACGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCGAGTATATCATATGATGAAATTAATAACTAT 180
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCAGAAACAGCTGTAT 240
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAsp--- 99
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTACTACGATGAGCGTCTGGGGCCAAAGG 360
Db 100 ---TTPGlyAsp-----SerLeuAspProTrpGlyLysGly 110
QY 361 ACCACGGTACCGCTCTCTCA 381
Db 111 ThrLeuValThrValSerSer 117

RESULT 3
Q9UD90 PRELIMINARY; PRT; 113 AA.
ID Q9UD90;
AC Q9UD90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_Like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D046D279 CRC64;

Alignment Scores:
Pred. No.: 1,37e-45 Length: 472
Score: 531.00 Matches: 101
Percent Similarity: 88.19% Conservative: 11
Best Local Similarity: 79.53% Mismatches: 11
Query Match: 76.29% Indels: 4
DB: 2 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x Q6N089 (1-472)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGATCCAGCGCTGGAGATCCCTGAGACTC 60
DB 20 GIVVAGLIneuValGInuSerGlyGlyGlyLeuValGInProGlyArgSerLeuArgLeu 39
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTATGAGCAATGAGTGGTCCGCAAGGCT 120
DB 40 SerCyAlaAlaSerGlyPheThrPheAspPtyrAlaMetHisrValArgGlnAla 59
QY 121 CCAGGCAAGGGCTGGAGTGGGTGGGAGCTATATCATATGATGAATATAATCTAT 180
DB 60 ProGlyLysGlyLeuGluTrpValSerGlyIleSerTrpAsnSerGlySerIleAlaTyr 79
QY 181 GCAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACGCTGTAT 240
DB 80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnGlyLysAsnSerLeuTyr 99
QY 241 CTCGAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTATTAATCTGTCGAAATATG 300
DB 100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrCysAlaLysGlnIle 119
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTAGGTATGACGTGGGGCCAAAGG 360
DB 120 GIVVAGLIneuValGInuSerGlyGlyGlyLeuValGInProGlyArgSerLeuArgLeu 135
QY 361 ACCAGCGTCAACGCTCTCTCA 381
DB 136 ThrThrValThrValSerSer 142

RESULT 6

Q8WU38 PRELIMINARY; PRT; 573 AA.

AC Q8WU38; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheafer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carlini P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malik J.A., Gumaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RM [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021276; AAH21276.1; --
DR PIR: S21205; S21205.
DR PIR: S30532; S30532.
DR HSSP: P18529; 118K.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Alignment Scores:
Pred. No.: 3,24e-45 Length: 573
Score: 527.50 Matches: 103
Percent Similarity: 87.40% Conservative: 8
Best Local Similarity: 81.10% Mismatches: 13
Query Match: 75.79% Indels: 3
DB: 2 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x Q8WU38 (1-573)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGATCCAGCGCTGGAGATCCCTGAGACTC 60
DB 20 GIVVAGLIneuValGInuSerGlyGlyGlyLeuValGInProGlyArgSerLeuArgLeu 39
QY 61 TCCTGTGACGCTCTGTGATTCACCTTCAGTATGAGCAATGAGTGGTCCGCAAGGCT 120
DB 40 SerCyAlaAlaSerGlyPheThrPheAspPtyrAlaMetHisrValArgGlnAla 59
QY 121 CCAGGCAAGGGCTGGAGTGGGTGGGAGCTATATCATATGATGAATATAATCTAT 180
DB 60 ProGlyLysGlyLeuGluTrpValSerGlyIleSerTrpAsnSerGlySerIleAlaTyr 79
QY 181 GCAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAACACGCTGTAT 240
DB 80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnGlyLysAsnSerLeuTyr 99
QY 241 CTCGAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTATTAATCTGTCGAAATATG 300
DB 100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrCysAlaLysGlnIle 118
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTAGGTATGACGTGGGGCCAAAGG 360
DB 119 -----GlySerGlySerTyrIleGlyTyrTyrTyrGlyMetAspValTrpGlyGlnGly 136

RESULT 7

HV3G_HUMAN STANDARD; PRT; 122 AA.

QY 361 ACCAGCGTCAACGCTCTCTCA 381
DB 137 ThrThrValThrValSerSer 143

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheafer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,


```
AC P01768;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN
  (1)
  SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
  location of a possible JH segment."
  Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MICELANUS; This mu chain was isolated from the plasma of a
  patient with macroglobulinemia.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00447; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyridone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyridone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Alignment Scores:
Pred. No.: 1,05e-44 Length: 122
Score: 521.50 Matches: 97
Percent Similarity: 86.05% Conservative: 14
Best Local Similarity: 75.19% Mismatches: 9
Query Match: 74.93% Indels: 9
DB: 1 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x HV3G_HUMAN (1-122)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTCAGCGCTGGAGGTCCTTGAGACTC 60
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValHisLeuValGlnSerGlyGlyValValValValValValValValValVal 20
QY 61 TCCGTGACGCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrlaMetHisTrpValArgGlnPro 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGAGTATATATATATATATATATATATATATATAT 180
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuAspTrpValAlaValIleSerIyr***Gly****LysTrpIyr 60
QY 181 GCAGACTCCGTTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGCAAGCTGTAT 240
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 Ala***SerValLysGlyArgPheThrIleSerArgAsp***SerLys***ThrLeuTrp 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGCTGTGTATTTACTGTGCAAGATATG 300
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetAsnSerLeuArgAlaGlu***ThrAlaValIyrTrpCysAlaArgAsp--- 99
QY 301 GGGTGGGGCAGTGGCTGAGAGCCCTACAC-----TACTACGGATATGAGTCTGGGGC 354
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 100 -----ArgProLeuTrpGly***IyrArgAlaAlaPheAsnTrpTrpGly 113
QY 355 CAAGGAGCACGCTCAGCTCTCTCTCA 381
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 114 GlnGlyThrLeuValThrValSerSer 122
```

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RESULT 8
QY509 PRELIMINARY; PRT; 147 AA.
AC QY509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
  Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
  myeloma using PCR with patient-specific immunoglobulin gene primers."
  Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig_v.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Alignment Scores:
Pred. No.: 2.78e-44 Length: 147
Score: 517.50 Matches: 99
Percent Similarity: 85.83% Conservative: 10
Best Local Similarity: 77.95% Mismatches: 17
Query Match: 74.35% Indels: 1
DB: 2 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x QY509 (1-147)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTCAGCGCTGGAGGTCCTTGAGACTC 60
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValHisLeuValGlnSerGlyGlyValValValValValValValValValVal 20
QY 61 TCCGTGACGCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCysGlnAlaSerGlyPheThrPheSerThrTrpIyrIleMetSerTrpValArgGlnAla 40
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGAGTATATATATATATATATATATATATATATAT 180
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuAspTrpValAlaValIleSerIyrAspGlySerThrGlnTrpIyr 60
QY 181 GCAGACTCCGTTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGCAAGCTGTAT 240
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AlaGlySerValLysGlyArgPheThrIleSerArgAspAsnSerIyrAsnThrLeuTrp 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGCAAGCTGTGTATTTACTGTGCAAGATATG 300
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetThrSerLeuArgValGlnAspThrAlaValIyrTrpCysAlaArgAspGly 100
QY 301 GGGTGGGGCAGTGGCTGAGAGCCCTACCTACTACTACTACTACTACTACTACTACTACT 360
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 101 AsnTrpPheAspSer---ValGlyTrpTrpIyrAlaGlyIleAspTrpTrpGlyGlnGly 119
QY 361 ACAAGGCTACCGTCTCTCTCA 381
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 120 ThrLeuValThrValSerSer 126

RESULT 9
Q6P181
```

OS-09-403-107-143_COPY1_1-381 (1-381) x Q6P181 (1-478)

ID	Q6P181	PRELIMINARY;	PRT;	478 AA.
AC	Q6P181			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Hom sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Hominidae; Homo			
OC	NCLTaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stedman M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,			
RA	Bromstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bohak S.A., McEwan P.C., McKernan K.J., Maller J.A., Gamarate P.H.,			
RA	Rodriguez A.C., Wotley E.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,			
RA	Villalón D.K., Muzny D.M., Sodegrién E.J., Lu X., Gibbs R.A.,			
RA	Faley J., Helton E., Kettman E., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Skalska D.E., Schenker A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: BC041037; AAH41037.1; -			
DR	HSSP: P01861; IADO.			
DR	InterPro: IPR003599; Ig			
DR	InterPro: IPR007110; Ig-like			
DR	InterPro: IPR003597; Ig-cl			
DR	InterPro: IPR003006; Ig_MHC			
DR	InterPro: IPR003596; Ig_v			
DR	Pfam: PF07654; Cl-set; 3.			
DR	SMART: SM00409; IG_2.			
DR	SMART: SM00407; IGcl; 3.			
DR	SMART: SM00406; IGv; 1.			
DR	PROSITE: PS50835; IG_LIKE; 4.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_2.			
KW	Hypothetical protein.			
SO	SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;			

Alignment Scores:			
Pred. No.:	3,77e-44	Length:	478
Score:	517.00	Matches:	102
Percent Similarity:	85.27%	Conservative:	8
Best Local Similarity:	79.07%	Mismatches:	17
Query Match:	74.28%	Indels:	2
DB:	2	Gaps:	1

QY	122	CCAGGCAAGGGCTGAGAGGGGTGGCACTTATCATATGATGGAATAATTAATCTAT	180		
Db	60	ProGlyLybGlyLyuGluIntPrValAlaAsnLLeysGlnAepGlySerGluLyTyTyTy	79		
QY	181	GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAGAAACAGCGTGTAT	240		
Db	80	ValAspSerValLybGlyAyrpGheThrLLeSerAyrAspAsnAlaYAsnSerLeuTy	99		
QY	241	CTGCAGTAATGAACAGCGCTGAGAGCTGAGAGCAACGCGTGCTGTTATCTGTGGAAAGATATG	300		
Db	100	LeuGlnMetAspSerLeuAyrGlnAlaGlnAspHnAlaValTyTyTyCybAlaAyrGluPhe	119		
QY	301	-----GGGTGGGGGCAAGTGGCTGAGAGACCTCACTACTACTACGATATGACGTCGTGGGC	354		
Db	120	GlusErThrMetThrValAlaAsnAlaAspTyTyTyTyPheTyTyMetAspValPrGly	139		
QY	355	CAAGGAGCCAGCGTCAACCGTCTCCCTCA	381		
Db	140	LybGlyThrThrValThrValSerSer	148		
RESULT 10					
ID	06RJ4	PRELIMINARY;	PRT: 470 AA.		
AC	Q6RJ4				
DT	05-JUL-2004	(Tremblrel. 27, Created)			
DT	05-JUL-2004	(Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004	(Tremblrel. 27, Last annotation update)			
DE	Hypotheetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,				
RA	Raha S.S., Locoallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bobak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunnaracne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Kryzhanietz M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RA	Strausberg R.;				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC018747; AAH18747.1; -				
DR	HSSP: P01861; IADO.				
DR	InterPro: IPR003599; IG.				
DR	InterPro: IPR007110; IG-like.				
DR	InterPro: IPR003597; IG_c1.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003596; IG_V.				
DR	Pfam: PF07654; Cl-secl; 3.				
DR	SMART: SMO0409; IG_2.				
DR	SMART: SMO0407; IGc1; 3.				
DR	SMART: SMO0406; IGv; 1.				
DR	PROSITE: PSS0835; IG_LIKE; 4.				

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein
 SQ SEQUENCE 470 AA; 5175 MW; 7849556A1FD7D9 CRC64;

Alignment Scores:
 Pred. No.: 1,666-42 Length: 470
 Score: 501.00 Matches: 100
 Percent Similarity: 81.89% Conservative: 4
 Best Local Similarity: 78.74% Mismatches: 17
 Query Match: 71.98% Indels: 6
 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x O6GM2 (1-470)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTGACGCTGCGAGGCTCTGAGACTC 60
 DB 20 GlnValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCCTGTGACGCTGCTGAGTTCACCTTACCTAGCTATGACGCTGCGGCGCGAGGCT 120
 DB 40 SerCysValValSerGlyPheThrPheSerSerTyrrPheSerSerTrpValArgGlnAla 59
 QY 121 CCAGGCAAGGGGCTGAGTGGTGGGACGTTATATCATATGATGAGTAATATATATAT 180
 DB 60 ProGlyIysGlyLeuGluTrpValAlaAlaSerGlyGlyAlaArgGlySerGluIysTyrr 79
 QY 181 GCAGACTCCGCTGAGAGGGCCGATTCACCATCTCCAGAGACATTCAGAGACGCTGTAT 240
 DB 80 ValAlaSerValIysGlyArgPheThrIleSerArgAspAlaIysAlaSerLeuTyrr 99
 QY 241 CTGCAAAAGAAACAGCTGAGCTGAGGACGAGGACGCGGTGTTACTGTGGCGAAAGATATG 300
 DB 100 LeuGlnMetAlaSerLeuArgAlaGluAspTrpAlaValIyrrTyrrCysAlaArgAsp 118
 QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGAGACGCTGGGGCCAGGCG 360
 DB 119 -----GlySerSerTrp-----TyrArgAspTrpPheAspProTrpGlyGlnGly 133
 QY 361 ACCAGGCTTCACCTGCTCTCTCA 381
 DB 134 ThrLeuValThrValSerSer 140

RESULT 11
 O6GM2 PRELIMINARY; PRT; 606 AA.

AC O6GM2; MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rabe S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Kuzny D.W., Sodergren B.V., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073758; AAH73758.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-sect; 4.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114F4C55 CRC64;

Alignment Scores:
 Pred. No.: 1,946-42 Length: 606
 Score: 500.50 Matches: 100
 Percent Similarity: 79.56% Conservative: 9
 Best Local Similarity: 72.99% Mismatches: 15
 Query Match: 71.91% Indels: 13
 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x O6GM2 (1-606)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGCTGACGCTGCGAGGCTCTGAGACTC 60
 DB 20 GlnValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCCTGTGACGCTGCTGAGTTCACCTTACCTAGCTATGAGTATGAGTATGAGTATGAGTAT 120
 DB 40 SerCysAlaAlaSerGlyPheThrPheSerAspTyrrPheSerSerTrpValArgGlnAla 59
 QY 121 CCAGGCAAGGGGCTGAGTGGTGGGACGTTATATCATATGATGAGTAATATATATAT 180
 DB 60 ProGlyIysGlyLeuGluTrpValSerTyrrIleSerSerSerSerTyrrThrAsnTyrr 79
 QY 181 GCAGACTCCGCTGAGAGGGCCGATTCACCATCTCCAGAGACATTCAGAGACGCTGTAT 240
 DB 80 ValAlaSerValIysGlyArgPheThrIleSerArgAspAlaIysAlaSerLeuTyrr 99
 QY 241 CTGCAAAAGAAACAGCTGAGCTGAGGACGAGGACGCGGTGTTACTGTGGCGAAAGATATG 300
 DB 100 LeuGlnMetAlaSerLeuArgAlaGluAspTrpAlaValIyrrTyrrCysAlaArgGly 118
 QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGAGACGCTGGGGCCAGGCG 360
 DB 119 -----GlySerSerTrp-----TyrArgAspTrpPheAspProTrpGlyGlnGly 136
 QY 361 TACTACGCTTACGCTGCTGAGTCTGGGGAGGCGCTGCTGACGCTGCGAGGCTCTGAGACTC 420
 DB 137 TyrTrpGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 153

RESULT 12
 O6MZU6 PRELIMINARY; PRT; 464 AA.

AC O6MZU6; MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686C15213.
 GN Name=DKFZp686C15213;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Oeanger A.,
RDO G., Han M., Wiemann S.,
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE4531.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-sect; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCAT2C6E8A0BC CRC64;

Alignment Scores:
Pred. No.: 2,09e-42 Length: 464
Score: 500.00 Matches: 97
Percent Similarity: 85.16% Conservative: 12
Best Local Similarity: 75.78% Mismatches: 9
Query Match: 71.84% Indels: 10
DB: Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x Q6MZD6 (1-464)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGGTCCAGGCTGGAGAGTCCCTGAGACTC 60
DB 20 GtUvaIgHleuValIgUserGlyGlyValGlnValIysProGlyIysSerIleuValGln 39
QY 61 TCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCCAGGCT 120
DB 40 SerCysAlaIaIaSerGlyPheThrPheSerSerTyIserMetAsnTrpValArgGlnAla 59
QY 121 CCAAGGCAAGGGGCTGGAGTGGGTGGGACGTATA---TCATATGATGGAATTAATAATAC 177
DB 60 ProGlyIysGlyLeuGlnTrpValSerSerPheSerSerArgIysSerTyIrgIuTyI 79
QY 178 TATGCAACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTG 237
DB 80 TyrAlaAspSerValIysGlyArgPheThrIleSerTrpAspAlaIysAsnSerIleu 99
QY 238 TATTCGCAATGAACACGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGAT 297
DB 100 TyrIleuGlnMetAsnSerIleuArgAlaGlnAsnThrAlaValTyTyTyCysAlaArgAsp 119
QY 298 ATGGGGTGGGGGCACTGCTGAGACCTTACTACTACTACGATATGACGCTGTGGGGCGCA 357
DB 120 LeuGlyTrp-----PheGlyLeuAspTyIrrpGlyGln 130
QY 358 GGGACGACGCTGACCGTCTCTCA 381
DB 131 GlyThrIleuValThrValSerSer 138

RESULT 13
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035030; AAD56266.1; -
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 122
FT 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Alignment Scores:
Pred. No.: 2.41e-42 Length: 122
Score: 498.50 Matches: 101
Percent Similarity: 84.25% Conservative: 6
Best Local Similarity: 79.53% Mismatches: 15
Query Match: 71.62% Indels: 5
DB: Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x Q9UL84 (1-122)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGGTCCAGGCTGGAGAGTCCCTGAGACTC 60
DB 1 GtUvaIgHleuValIgUserGlyGlyValGlnValIysProGlyIysSerIleuValGln 20
QY 61 TCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyIserMetAsnTrpValArgGlnAla 40
QY 121 CCAAGGCAAGGGGCTGGAGTGGGTGGGACGTATATCATATGATGGAATTAATAATCTAT 180
DB 41 ProGlyIysGlyLeuGlnTrpValAlaIaIaIleSerTrpAsnAspGlySerAsnIysPheTy 60
QY 181 GCAAGATCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGAACAGCGCTAT 240
DB 61 AlaAspSerValIysGlyArgPheThrIlePheArgAspAsnSerTyAsnMetCasp 80
QY 241 CTGCAATGAACACGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGTATG 300
DB 81 LeuGlnMetAsnSerIleuArgAlaGlnAsnThrAlaValTyTyTyCysAlaArgAsp--- 99
QY 301 GGGTGGGGGCACTGCTGAGACCTTACTACTACTACGATATGACGCTGTGGGGCGCAAGG 360
DB 100 -----GluArgGlyArgLeuValGlyThrTyPhe-----AspTyTrpGlyGlnI 115
QY 361 ACCACGCTACCGTCTCTCA 381
DB 116 ThrIleuValThrValSerSer 122

RESULT 14
Q6RP95 PRELIMINARY; PRT; 544 AA.
AC Q6RP95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

US-09-403-107-143_COPY_1_381 (1-381) x Q96BB9 (1-597)

```

QY      1 GAGGTGAGCTGCTCGAGTCTGGGGAGAGGCTGTGGTCCAGCCTGGAGGCTCCCTGAGACTC 60
      |||
Db      20 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
      |||
QY      61 TCCGTGTCAGCCTCTGGATTCACTTCAGTAGCTATGATGCATGCACTGGTCCGCCAGGCT 120
      |||
Db      40 SerCysAlaAlaSerGlyPheSerPheSerSerTyrAlaMetValentpValArgGlnAla 59
      |||
QY      121 CCAAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTAT 180
      |||
Db      60 ProGlyLysGlyLeuGlnuTTPValSerAlaIleSerGlySerGlySerThrTyrTyr 79
      |||
QY      181 GCAGACTCCCTGAAAGGGCCGATTCAACATCTCCAGAGACAAATCCAAAGAACAGCTGTAT 240
      |||
Db      80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeuTyr 99
      |||
QY      241 CTCCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAGAT--- 297
      |||
Db      100 LeuGlnMetAsnSerLeuAlaGlnAspThrAlaValTyrTyrCysAlaIysAspPro 119
      |||
QY      298 ATGGGGTGGGGCAGTGGCTGGAGACCTCTACTACTACTACGGTATGACGCTGGGGCCAA 357
      |||
Db      120 ArgGlyTyrSerAlaSerGlyAsn-----TyrThrArgGlnuAspTyrTTPGlyGln 136
      |||
QY      358 GGGACCAACGGTCAACCTCTCTCTCA 381
      |||
Db      137 GlyThrLeuValThrValSerSer 144

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Search completed: August 29, 2005, 11:06:48
Job time : 84.1389 secs